



SEQUENCE LISTING

10> Kato, Seishi
Sekine, Shingo
Kimura, Tomoko

<120> HUMAN PROTEINS HAVING TRANSMEMBRANE
DOMAINS AND DNAS ENCODING THESE PROTEINS

<130> GIN-6706CPUS

<140> 09/445,258

<141> 1999-12-01

<150> PCT/US98/02445

<151> 1998-06-03

<150> JP 9-144948

<151> 1997-06-03

<160> 67

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 382

<212> PRT

<213> Homo sapiens

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Gly	Ala	Met	Ser	Pro	Pro	Gln	Leu	Ala	Leu	Asn	Pro	Ser	Ala	Leu	Leu	20	25	30	
Ser	Arg	Gly	Cys	Asn	Asp	Ser	Asp	Val	Leu	Ala	Val	Ala	Gly	Phe	Ala	35	40	45	
Leu	Arg	Asp	Ile	Asn	Lys	Asp	Arg	Lys	Asp	Gly	Tyr	Val	Leu	Arg	Leu	50	55	60	
Asn	Arg	Val	Asn	Asp	Ala	Gln	Glu	Tyr	Arg	Arg	Gly	Gly	Leu	Gly	Ser	65	70	75	80
Leu	Phe	Tyr	Leu	Thr	Leu	Asp	Val	Leu	Glu	Thr	Asp	Cys	His	Val	Leu	85	90	95	
Arg	Lys	Lys	Ala	Trp	Gln	Asp	Cys	Gly	Met	Arg	Ile	Phe	Phe	Glu	Ser	100	105	110	
Val	Tyr	Gly	Gln	Cys	Lys	Ala	Ile	Phe	Tyr	Met	Asn	Asn	Pro	Ser	Arg	115	120	125	
Val	Leu	Tyr	Leu	Ala	Ala	Tyr	Asn	Cys	Thr	Leu	Arg	Pro	Val	Ser	Lys	130	135	140	
Lys	Lys	Ile	Tyr	Met	Thr	Cys	Pro	Asp	Cys	Pro	Ser	Ser	Ile	Pro	Thr	145	150	155	160
Asp	Ser	Ser	Asn	His	Gln	Val	Leu	Glu	Ala	Ala	Thr	Glu	Ser	Leu	Ala	165	170	175	
Lys	Tyr	Asn	Asn	Glu	Asn	Thr	Ser	Lys	Gln	Tyr	Ser	Leu	Phe	Lys	Val	180	185	190	
Thr	Arg	Ala	Ser	Ser	Gln	Trp	Val	Val	Gly	Pro	Ser	Tyr	Phe	Val	Glu	195	200	205	
Tyr	Leu	Ile	Lys	Glu	Ser	Pro	Cys	Thr	Lys	Ser	Gln	Ala	Ser	Ser	Cys	210	215	220	
Ser	Leu	Gln	Ser	Ser	Asp	Ser	Val	Pro	Val	Gly	Leu	Cys	Lys	Gly	Ser	225	230	235	240

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$\langle 400 \rangle$ 2

2

	275		280		285
Phe	Phe Phe Ile Pro Leu Ser Tyr Leu Pro Thr Ser Leu Ala Asp Tyr				
	290		295		300
Ile	Leu Thr Arg Ser Trp Pro Lys Pro Ala Gln Ala Val				
305		310		315	

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 <213> Homo sapiens

<400> 3

Met	Ser	Asp	Ser	Lys	Glu	Pro	Arg	Val	Gln	Gln	Leu	Gly	Leu	Leu	Gly
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Cys	Leu	Gly	His	Gly	Ala	Leu	Val	Leu	Gln	Leu	Leu	Ser	Phe	Met	Leu
			20					25					30		
Leu	Ala	Gly	Val	Leu	Val	Ala	Ile	Leu	Val	Gln	Val	Ser	Lys	Val	Pro
			35				40						45		
Ser	Ser	Leu	Ser	Gln	Glu	Gln	Ser	Glu	Gln	Asp	Ala	Ile	Tyr	Gln	Asn
	50				55					60					
Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Ser	Glu	Lys	Ser	Lys
65				70					75						80
Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly
			85					90						95	
Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr
			100					105					110		
Arg	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln
		115				120						125			
Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Arg	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu
	130				135						140				
Pro	Glu	Lys	Ser	Lys	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Arg	Leu
145				150					155						160
Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln	Glu	Ile
			165					170						175	
Tyr	Gln	Glu	Leu	Thr	Glu	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu
			180				185						190		
Lys	Ser	Lys	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Gln	Leu	Lys	Ala
	195					200						205			
Ala	Val	Gly	Glu	Leu	Pro	Asp	Gln	Ser	Lys	Gln	Gln	Gln	Ile	Tyr	Gln
	210				215							220			
Glu	Leu	Thr	Asp	Leu	Lys	Thr	Ala	Phe	Glu	Arg	Leu	Cys	Arg	His	Cys
225				230					235						240
Pro	Lys	Asp	Trp	Thr	Phe	Phe	Gln	Gly	Asn	Cys	Tyr	Phe	Met	Ser	Asn
			245					250					255		
Ser	Gln	Arg	Asn	Trp	His	Asp	Ser	Val	Thr	Ala	Cys	Gln	Glu	Val	Arg
		260					265						270		
Ala	Gln	Leu	Val	Val	Ile	Lys	Thr	Ala	Glu	Glu	Gln	Leu	Pro	Ala	Val
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Leu	Glu	Gln	Trp	Arg	Thr	Gln	Gln								
	290					295									

<210> 4
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 <213> Homo sapiens

<400> 4

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1				5					10					15	

Leu Cys Leu Val Cys Ile Val Ala Asn Ala Leu Leu Leu Val Pro Asn
20 25 30
Gly Glu Thr Ser Trp Thr Asn Thr Asn His Leu Ser Leu Gln Val Trp
35 40 45
Leu Met Gly Gly Phe Ile Gly Gly Gly Leu Met Val Leu Cys Pro Gly
50 55 60
Ile Ala Ala Val Arg Ala Gly Gly Lys Gly Cys Cys Gly Ala Gly Cys
65 70 75 80
Cys Gly Asn Arg Cys Arg Met Leu Arg Ser Val Phe Ser Ser Ala Phe
85 90 95
Gly Val Leu Gly Ala Ile Tyr Cys Leu Ser Val Ser Gly Ala Gly Leu
100 105 110
Arg Asn Gly Pro Arg Cys Leu Met Asn Gly Glu Trp Gly Tyr His Phe
115 120 125
Glu Asp Thr Ala Gly Ala Tyr Leu Leu Asn Arg Thr Leu Trp Asp Arg
130 135 140
Cys Glu Ala Pro Pro Arg Val Val Pro Trp Asn Val Thr Leu Phe Ser
145 150 155 160
Leu Leu Val Ala Ala Ser Cys Leu Glu Ile Val Leu Cys Gly Ile Gln
165 170 175
Leu Val Asn Ala Thr Ile Gly Val Phe Cys Gly Asp Cys Arg Lys Lys
180 185 190
Gln Asp Thr Pro His
195

<210> 5
<211> 221
<212> PRT
<213> Homo sapiens

<400> 5
Met Glu Ala Gly Gly Phe Leu Asp Ser Leu Ile Tyr Gly Ala Cys Val
1 5 10 15
Val Phe Thr Leu Gly Met Phe Ser Ala Gly Leu Ser Asp Leu Arg His
20 25 30
Met Arg Met Thr Arg Ser Val Asp Asn Val Gln Phe Leu Pro Phe Leu
35 40 45
Thr Thr Glu Val Asn Asn Leu Gly Trp Leu Ser Tyr Gly Ala Leu Lys
50 55 60
Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu Gln
65 70 75 80
Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg Val
85 90 95
Val Leu Leu Gln Thr Ala Thr Leu Leu Gly Val Leu Leu Leu Gly Tyr
100 105 110
Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro Glu Ala Arg Leu Gln Gln
115 120 125
Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser Pro
130 135 140
Leu Ala Asp Leu Ala Lys Val Ile Gln Thr Lys Ser Thr Gln Cys Leu
145 150 155 160
Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu Thr Ser Ala Ser Trp Cys
165 170 175
Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Met Val Ser Asn Phe
180 185 190
Pro Gly Ile Val Thr Ser Phe Ile Arg Phe Trp Leu Phe Trp Lys Tyr
195 200 205
Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu Leu Gln Thr
210 215 220

<210> 6
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 <213> Homo sapiens

<400> 6
 Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala Ile Thr Arg
 1 5 10 15
 Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly Lys Leu Gly
 20 25 30
 Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala Phe Leu Tyr
 35 40 45
 Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr Phe Pro Val
 50 55 60
 Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr Phe Leu Tyr
 65 70 75 80
 Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly Arg Pro Ala
 85 90 95
 Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile Val Ile Thr
 100 105 110
 Gly Leu Ala Met Asp Met Gln Leu Met Ile Pro Leu Ile Met Ser
 115 120 125
 Leu Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile Val Ser Phe
 130 135 140
 Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp Val Ile Leu
 145 150 155 160
 Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu Leu Ile Gly
 165 170 175
 Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg Tyr Pro Met
 180 185 190
 Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe Leu Tyr Arg
 195 200 205
 Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly Val Pro Pro
 210 215 220
 Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly Gly Arg His
 225 230 235 240
 Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln
 245 250

<210> 7
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 <213> Homo sapiens

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 Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro Ser
 1 5 10 15
 Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn Pro
 20 25 30
 Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro Val
 35 40 45
 Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Leu Thr Tyr Gly Leu
 50 55 60
 Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met Arg
 65 70 75 80
 Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu Gly
 85 90 95
 Leu Ala Val Thr Ala Met Lys Ser Arg Pro
 100 105

<210> 8
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 <213> Homo sapiens

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 Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly Ser
 1 5 10 15
 Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu Lys Glu
 20 25 30
 Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu Glu Leu Leu
 35 40 45
 Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly Thr Ser Val Thr
 50 55 60
 Leu His His Ala Arg Ser Gln His His Val Val Cys Asn Thr
 65 70 75

<210> 9
 <211> 314
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 <213> Homo sapiens

<400> 9
 Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly
 1 5 10 15
 Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly
 20 25 30
 Gln Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala
 35 40 45
 Gln Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro
 50 55 60
 Arg Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala
 65 70 75 80
 Gln Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val
 85 90 95
 Ile Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His
 100 105 110
 Leu Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Lys Leu Glu Glu Lys
 115 120 125
 Gln Ala Arg Lys Ala Gln Arg Glu Ala Glu Glu Ala Glu Arg Glu Glu
 130 135 140
 Arg Lys Arg Leu Glu Ser Gln Arg Glu Ala Glu Trp Lys Lys Glu Glu
 145 150 155 160
 Glu Arg Leu Arg Leu Glu Glu Glu Gln Lys Glu Glu Glu Glu Arg Lys
 165 170 175
 Ala Arg Glu Glu Gln Ala Gln Arg Glu His Glu Glu Tyr Leu Lys Leu
 180 185 190
 Lys Glu Ala Phe Val Val Glu Glu Gly Val Gly Glu Thr Met Thr
 195 200 205
 Glu Glu Gln Ser Gln Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys
 210 215 220
 Gln Ser Lys Val Val Leu Leu Glu Asp Leu Ala Ser Gln Val Gly Leu
 225 230 235 240
 Arg Thr Gln Asp Thr Ile Asn Arg Ile Gln Asp Leu Leu Ala Glu Gly
 245 250 255
 Thr Ile Thr Gly Val Ile Asp Asp Arg Gly Lys Phe Ile Tyr Ile Thr
 260 265 270
 Pro Glu Glu Leu Ala Ala Val Ala Asn Phe Ile Arg Gln Arg Gly Arg

275 280 285
Val Ser Ile Ala Glu Leu Ala Gln Ala Ser Asn Ser Leu Ile Ala Trp
290 295 300
Gly Arg Glu Ser Pro Ala Gln Ala Pro Ala
305 310

<210> 10
<211> 195
<212> PRT
<213> Homo sapiens

<400> 10
Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu
1 5 10 15
Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
20 25 30
Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
35 40 45
Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp Asp Glu Pro Pro Pro
50 55 60
Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg
65 70 75 80
Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys
85 90 95
Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro
100 105 110
Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
115 120 125
Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp
130 135 140
Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp Trp Glu Ser Gln Phe
145 150 155 160
Thr Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu
165 170 175
Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ala Arg
180 185 190
Lys Asn Asp
195

<210> 11
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<213> Homo sapiens

<400> 11
Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu Val
1 5 10 15
Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala Gly Ile
20 25 30
Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile
35 40 45
Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn Leu His Glu Arg
50 55 60
Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu Val Val Ser
65 70 75 80
Leu Gly Thr Val Asp Val Leu Lys Gln His Ile Asn Pro Asn Lys Thr
85 90 95
Leu Asp Pro Phe Glu Thr Met Leu Lys Ser Leu Leu Arg Tyr Gln Ser
100 105 110

Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn	His	Met	Arg	Lys	Lys	Leu	Tyr	Glu		
	115						120					125					
Asn	Gly	Val	Thr	Asp	Ser	Leu	Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys		
	130						135				140						
Leu	Ser	Glu	Glu	Leu	Leu	Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln		
	145					150				155					160		
His	Val	Pro	Leu	Ser	Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val		
			165						170					175			
Thr	Gln	Met	Val	Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile		
			180						185					190			
Arg	Phe	Gln	Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly		
	195						200					205					
Phe	Leu	Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr		
	210						215					220					
Glu	Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys		
	225					230					235				240		
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser	Leu		
				245					250					255			
Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser	Met	Ile		
			260						265					270			
Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys	Thr	Trp	Ala		
	275							280				285					
Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	Lys	Leu	Tyr	Glu		
	290						295				300						
Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	Thr	Pro	Glu	Lys	Ile		
	305					310					315				320		
Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	Cys	Glu	Thr	Val	Arg	Thr		
				325						330				335			
Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	Leu	Gln	Asp	Ile	Glu	Gly	Lys		
			340						345					350			
Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu		
	355						360					365					
Gly	Val	Val	Leu	Gln	Asp	Pro	Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe		
	370						375					380					
Asp	Pro	Asp	Arg	Phe	Asp	Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser		
	385					390					395				400		
Leu	Gly	Phe	Ser	Gly	Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr		
				405					410					415			
Met	Val	Thr	Thr	Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu		
			420						425					430			
Leu	Ser	Val	Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr		
		435							440					445			
Ser	Ser	Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr				
	450						455					460					

<210> 12
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 <213> Homo sapiens

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 Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro
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 20 25 30
 Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu
 35 40 45
 Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
 50 55 60
 Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val

65					70					75					80
Leu	Leu	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	Tyr	Lys	Leu	Leu	Lys	Lys
				85					90					95	
Ala	Asp	Glu	Gly	Leu	Ala	Ser	Leu	Ser	Glu	Asp	Gly	Arg	Ser	Pro	Ile
			100						105					110	
Ser	Ile	Arg	Gln	Met	Ala	Tyr	Val	Ser	Gly	Leu	Ser	Phe	Gly	Ile	Ile
		115					120					125			
Ser	Gly	Val	Phe	Ser	Val	Ile	Asn	Ile	Leu	Ala	Asp	Ala	Leu	Gly	Pro
	130					135					140				
Gly	Val	Val	Gly	Ile	His	Gly	Asp	Ser	Pro	Tyr	Tyr	Phe	Leu	Thr	Ser
145				150					155					160	
Ala	Phe	Leu	Thr	Ala	Ala	Ile	Ile	Leu	Leu	His	Thr	Phe	Trp	Gly	Val
				165					170					175	
Val	Phe	Phe	Asp	Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	Ala	Leu	Gly	Leu
			180					185					190		
Val	Val	Gly	Ser	His	Leu	Leu	Thr	Ser	Gly	Leu	Thr	Phe	Leu	Asn	Pro
	195					200						205			
Trp	Tyr	Glu	Ala	Ser	Leu	Leu	Pro	Ile	Tyr	Ala	Val	Thr	Val	Ser	Met
	210				215						220				
Gly	Leu	Trp	Ala	Phe	Ile	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Ser	Ile	Gln
225					230				235					240	
Arg	Ser	Leu	Leu	Cys	Lys	Asp									
				245											

<210> 13
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 <212> PRT
 <213> Homo sapiens

<400> 13

Met	Asn	Phe	Tyr	Leu	Leu	Leu	Ala	Ser	Ser	Ile	Leu	Cys	Ala	Leu	Ile
1				5					10					15	
Val	Phe	Trp	Lys	Tyr	Arg	Arg	Phe	Gln	Arg	Asn	Thr	Gly	Glu	Met	Ser
			20				25					30			
Ser	Asn	Ser	Thr	Ala	Leu	Ala	Leu	Val	Arg	Pro	Ser	Ser	Ser	Gly	Leu
		35				40					45				
Ile	Asn	Ser	Asn	Thr	Asp	Asn	Asn	Leu	Ala	Val	Tyr	Asp	Leu	Ser	Arg
	50				55					60					
Asp	Ile	Leu	Asn	Asn	Phe	Pro	His	Ser	Ile	Ala	Arg	Gln	Lys	Arg	Ile
65				70					75					80	
Leu	Val	Asn	Leu	Ser	Met	Val	Glu	Asn	Lys	Leu	Val	Glu	Leu	Glu	His
			85					90					95		
Thr	Leu	Leu	Ser	Lys	Gly	Phe	Arg	Gly	Pro	Ser	Pro	His	Arg	Lys	Ser
			100					105					110		

Thr

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 <212> PRT
 <213> Homo sapiens

<400> 14

Met	Gly	Arg	Trp	Ala	Leu	Asp	Val	Ala	Phe	Leu	Trp	Lys	Ala	Val	Leu
1				5				10						15	
Thr	Leu	Gly	Leu	Val	Leu	Leu	Tyr	Tyr	Cys	Phe	Ser	Ile	Gly	Ile	Thr
		20					25					30			
Phe	Tyr	Asn	Lys	Trp	Leu	Thr	Lys	Ser	Phe	His	Phe	Pro	Leu	Phe	Met
		35				40						45			

Thr	Met	Leu	His	Leu	Ala	Val	Ile	Phe	Leu	Phe	Ser	Ala	Leu	Ser	Arg	
50						55					60					
Ala	Leu	Val	Gln	Cys	Ser	Ser	His	Arg	Ala	Arg	Val	Val	Leu	Ser	Trp	
65					70					75					80	
Ala	Asp	Tyr	Leu	Arg	Arg	Val	Ala	Pro	Thr	Ala	Leu	Ala	Thr	Ala	Leu	
				85					90					95		
Asp	Val	Gly	Leu	Ser	Asn	Trp	Ser	Phe	Leu	Tyr	Val	Thr	Val	Ser	Leu	
		100						105					110			
Tyr	Thr	Met	Thr	Lys	Ser	Ser	Ala	Val	Leu	Phe	Ile	Leu	Ile	Phe	Ser	
	115						120					125				
Leu	Ile	Phe	Lys	Leu	Glu	Glu	Leu	Arg	Ala	Ala	Leu	Val	Leu	Val	Val	
	130					135					140					
Leu	Leu	Ile	Ala	Gly	Gly	Leu	Phe	Met	Phe	Thr	Tyr	Lys	Ser	Thr	Gln	
145					150					155					160	
Phe	Asn	Val	Glu	Gly	Phe	Ala	Leu	Val	Leu	Gly	Ala	Ser	Phe	Ile	Gly	
			165						170					175		
Gly	Ile	Arg	Trp	Thr	Leu	Thr	Gln	Met	Leu	Leu	Gln	Lys	Ala	Glu	Leu	
	180						185						190			
Gly	Leu	Gln	Asn	Pro	Ile	Asp	Thr	Met	Phe	His	Leu	Gln	Pro	Leu	Met	
	195						200					205				
Phe	Leu	Gly	Leu	Phe	Pro	Leu	Phe	Ala	Val	Phe	Glu	Gly	Leu	His	Leu	
	210					215					220					
Ser	Thr	Ser	Glu	Lys	Ile	Phe	Arg	Phe	Gln	Asp	Thr	Gly	Leu	Leu	Leu	
225					230					235					240	
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			245						250					255		
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		260						265					270			
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	275						280					285				
His	Leu	Leu	Gly	Asp	Gln	Ile	Ser	Leu	Leu	Asn	Trp	Leu	Gly	Phe	Ala	
	290					295					300					
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				310						315					320	
Ser	Arg	Gly	Asp	Gly	Gly	Pro	Lys	Ala	Leu	Lys	Gly	Leu	Gly	Ser	Ser	
			325						330					335		
Pro	Asp	Leu	Glu	Leu	Leu	Leu	Arg	Ser	Ser	Gln	Arg	Glu	Glu	Gly	Asp	
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<210> 15
 <211> 226
 <212> PRT
 <213> Homo sapiens

<400> 15

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		35					40						45			
Ile	Phe	Ile	Thr	Tyr	Gly	Leu	Phe	Arg	Gly	Glu	Ser	Ser	Glu	Glu	Leu	
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Ser	His	Gly	Leu	Ala	Glu	Pro	Lys	Lys	Lys	Phe	Ala	Val	Leu	Glu	Ile	
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			85						90					95		
Leu	Val	Leu	Ser	Leu	Ile	Thr	Ser	Leu	Leu	Ser	Ser	Gly	Phe	Thr	Phe	

			100					105					110			
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		130					135					140				
Ile	Leu	Phe	Val	Ala	Asn	Thr	Gln	Ser	Asn	Gln	Leu	Ser	Glu	Glu	Leu	
145					150					155					160	
Phe	Gln	Met	Leu	Tyr	Pro	Ala	Thr	Thr	Ser	Lys	Gly	Thr	Thr	His	Ser	
				165					170					175		
Tyr	Gly	Tyr	Ser	Phe	Trp	Leu	Ile	Leu	Leu	Val	Ile	Leu	Leu	Asn	Ile	
			180					185					190			
Val	Thr	Val	Thr	Ile	Ile	Ile	Phe	Tyr	Gln	Lys	Ala	Arg	Tyr	Gln	Arg	
		195					200					205				
Lys	Gln	Glu	Gln	Arg	Lys	Pro	Met	Glu	Tyr	Ala	Pro	Arg	Asp	Gly	Ile	
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Leu	Phe															
225																

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 <212> PRT
 <213> Homo sapiens

<400> 16

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Thr	Ala	Pro	Cys	Ser	Arg	Gly	Ser	Trp	Ser	Ala	Asp	Leu	Asp	Lys		
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Cys	Met	Asp	Cys	Ala	Ser	Cys	Arg	Ala	Arg	Pro	His	Ser	Asp	Phe	Cys	
	50					55					60					
Leu	Gly	Cys	Ala	Ala	Ala	Pro	Pro	Ala	Pro	Phe	Arg	Leu	Leu	Trp	Pro	
65				70						75				80		
Ile	Leu	Gly	Gly	Ala	Leu	Ser	Leu	Thr	Phe	Val	Leu	Gly	Leu	Leu	Ser	
			85					90					95			
Gly	Phe	Leu	Val	Trp	Arg	Arg	Cys	Arg	Arg	Arg	Glu	Lys	Phe	Thr	Thr	
		100					105						110			
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Gln																

<210> 17
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 17

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		20						25					30			
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Glu	Thr	Ser	Val	Glu	Ser	Ala	Val	Asp	Thr	Pro	Phe	Pro	Ala	Gly	Ile	
	50					55					60					
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<211> 193
<212> PRT
<213> Homo sapiens
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[illegible]

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<211> 1146
<212> DNA
<213> Homo sapiens
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ccagtttcaa aaaaaaagat ttacatgacg tgccttgact gcccaagctc catacccact 480
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gagaacacat ccaagcagta ttctctcttc aaagtcacca gggcttctag ccagtgggtg 600
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<210> 20
 <211> 951
 <212> DNA
 <213> Homo sapiens

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ctgacggaga agggggccga gcagctgagg ggcagacgt ctgacaggct ggagacggtg 240
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tattcagctg gctgggatgc taaatttttc ttcacccctc tatcttattt acctacatca 900
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<210> 21
 <211> 888
 <212> DNA
 <213> Homo sapiens

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tggcacgact ccgtcaccgc ctgccaggaa gtgaggggcc agctcgtcgt aatcaaaact 840
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<210> 22
 <211> 591

<212> DNA
<213> Homo sapiens

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<210> 23
<211> 663
<212> DNA
<213> Homo sapiens

<400> 23
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<210> 24
<211> 753
<212> DNA
<213> Homo sapiens

<400> 24
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tocacacctc agtttttgta ccgctggctg ccagtagga gaggaggagt atcaggattt 660
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<210> 25
<211> 318
<212> DNA
<213> Homo sapiens

<400> 25
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acctacggcc	tctactcctt	ccaccggggc	aacagccagc	gctctcagct	catgatgcgc	240
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<210> 26
 <211> 234
 <212> DNA
 <213> Homo sapiens

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gagtcagct	tcctggaatt	gcttgaaaag	ctctgcctcc	tcctccatct	cccttcagg	180
accagcgtca	ccctccacca	tgcaagatct	caacaccatg	ttgtctgcaa	caca	234

<210> 27
 <211> 942
 <212> DNA
 <213> Homo sapiens

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<210> 28
 <211> 585
 <212> DNA
 <213> Homo sapiens

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<210> 29
 <211> 1386
 <212> DNA
 <213> Homo sapiens

<400> 29

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<210> 30

<211> 741

<212> DNA

<213> Homo sapiens

<400> 30

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gaccggctag atgcccggt ccagtagcgg ctctctgatt ttgggtgctg tgtctctgtc 240
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<210> 31

<211> 339

<212> DNA

<213> Homo sapiens

<400> 31

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gtgagaccct cttcttctgg gtttaattaac agcaatacag acaacaatct tgcagtctac 180
gacctctctc gggatatttt aaataatttc ccacactcaa tagccaggca gaagcgaata 240
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aagggtttca gaggtgcatc acctcaccgg aaatccacc 339

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<210> 32

<211> 1095
 <212> DNA
 <213> Homo sapiens

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 agcttccatt tccccctctt catgacgatg ctgcacctgg ccgtgatctt cctcttctcc 180
 gccctgtcca gggcgctggt tcagtgtctc agccacaggg cccgtgtggt gctgagctgg 240
 gccgactacc tcagaagagt ggctcccaca gctctggcga cggcgcttga cgtgggcttg 300
 tccaactgga gcttctgtta tgtcacctgc tcgctgtaca caatgaccaa atcctcagct 360
 gtctcttcca tcttgatctt ctctctgate ttcaagctgg aggagctgcg cgcggcactg 420
 gtcttggtgg tcctcctcat cgccgggggt ctcttcatgt tcacctacaa gtccacacag 480
 ttcaacgtgg agggcttcgc cttggtgctg ggggcctcgt tcacggtgg cattcgctgg 540
 accctcacc agatgctcct gcagaaggct gaactcggcc tccagaatcc catcgacacc 600
 atgttccacc tgcagccact catgttctct gggctcttcc ctctctttgc tgtatttgaa 660
 ggtctccatt tgtccacatc tgagaaaatc ttccgtttcc aggacacagg gctgctcctg 720
 cgggtacttg ggagcctctt ccttggcggg attctcgcct ttggtttggg cttctctgag 780
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 tccagaggtg atggtggccc caaggccttg aaggggctgg gctccagccc cgacctggag 1020
 ctgctgctcc ggagcagcca gcgggaggaa ggtgacaatg aggaggagga gtactttgtg 1080
 gccagggggc agcag 1095

<210> 33
 <211> 678
 <212> DNA
 <213> Homo sapiens

<400> 33
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 agagactctg cttcaaatgg gagcattttc atcacttacg gactttttcg tggggagagt 180
 agtgaagaat tgagtcacgg acttgacaga ccaaagaaaa agtttgcagt tttagagata 240
 ctgaataatt cttcccaaaa aactctgcat tcgggtgacta tcctgttctt ggtcctgagt 300
 ttgatcacgt cgctgctgag ctctgggttt accttctaca acagcatcag caacccttac 360
 cagacattcc tggggccgac gggggtgtac acctggaacg ggctcgggtc atccttcgtt 420
 tttgtgacca tgatactgtt tgtggcgaac acgcagtcca accaactctc cgaagagttg 480
 ttccaaatgc tttaccgggc aaccaccagt aaaggaacga cccacagtta cggatactcg 540
 ttctggctca tactgctcgt cattcttcta aatatagtca ctgtaaccat catcattttc 600
 taccagaagg ccagatacca gcggaagcag gagcagagaa agccaatgga atatgctcca 660
 agggacggaa ttttatcc 678

<210> 34
 <211> 387
 <212> DNA
 <213> Homo sapiens

<400> 34
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 ttgctgcgct ccgtggccgg ggagcaagcg ccaggcaccg cccctgctc ccgcggcagc 120
 tcctggagcg cggacctgga caagtgcagt gactgcgcgt cttgcagggc gcgaccgcac 180
 agcgaattct gcctgggctg cgctgcagca cctcctgcc ccttcggct gctttggccc 240
 atccttgggg gcgctctgag cctgaccttc gtgctggggc tgctttcttg ctttttggtc 300
 tggagacgat gccgcaggag agagaagttc accaccccca tagaggagac cggcggagag 360
 ggctgcccag ctgtggcgct gatccag 387

<210> 35
 <211> 489
 <212> DNA

<213> Homo sapiens

<400> 35

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ccgcccgtgc agtgggcctt ccaggagacc agtgtggaga gcgccgtgga cacgcccttc 180
ccagctggaa tatttgtgag gctggaattt aagctgcagc agacaagctg ccggaagagg 240
gactggaaga aacccgagtg caaagtcagg cccaatggga ggaaacggaa atgcctggcc 300
tgcataaac tgggctctga ggacaaagtt ctgggcccgt tggctcactg ccccatagag 360
acccaagttc tgcgggagcg tgaggagcac caggagaccc agtgcctcag ggtgcagcgg 420
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ccccgcagc                                     489

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<210> 36

<211> 579

<212> DNA

<213> Homo sapiens

<400> 36

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agcgccatcg ccttcgacat catcgcgctg gccggccgcg gctggttgca gtctagcgac 120
cacggccaga cgtcctcgct gtggtggaaa tgctcccaag agggcggcgg cagcgggtcc 180
tacgaggagg gctgtcagag cctcatggag tacgcgtggg gtagagcagc ggctgccatg 240
ctcttctgtg gcttcacat cctggtgatc tgtttcatcc tctccttctt cgccctctgt 300
ggaccccaga tgcttgtctt cctgagagtg attggaggtc tccttgccctt ggctgctgtg 360
ttccagatca tctccctggg aatttacccc gtgaagtaca cccagacctt cacccttcat 420
gccaacctgt ctgtcactta catctataac tgggcctacg gctttgggtg ggcagccacg 480
attatcctga tcggctgtgc cttcttcttc tgcctgcctc ccaactacga agatgacctt 540
ctgggcaatg ccaagcccag gtacttctac acatctgcc                                     579

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<210> 37

<211> 1502

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (37)...(1185)

<400> 37

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                                         Met Gly Leu Leu Leu Pro
                                         1                               5

ctg gca ctc tgc atc cta gtc ctg tgc tgc gga gca atg tct cca ccc 102
Leu Ala Leu Cys Ile Leu Val Leu Cys Cys Gly Ala Met Ser Pro Pro
          10                      15                      20

cag ctg gcc ctc aac ccc tcg gct ctg ctc tcc cgg ggc tgc aat gac 150
Gln Leu Ala Leu Asn Pro Ser Ala Leu Leu Ser Arg Gly Cys Asn Asp
          25                      30                      35

tcc gat gtg ctg gca gtt gca ggc ttt gcc ctg cgg gat att aac aaa 198
Ser Asp Val Leu Ala Val Ala Gly Phe Ala Leu Arg Asp Ile Asn Lys
          40                      45                      50

gac aga aag gat ggc tat gtg ctg aga ctc aac cga gtg aac gac gcc 246
Asp Arg Lys Asp Gly Tyr Val Leu Arg Leu Asn Arg Val Asn Asp Ala
          55                      60                      65                      70

cag gaa tac aga cgg ggt ggc ctg gga tct ctg ttc tat ctt aca ctg 294

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Gln	Glu	Tyr	Arg	Arg	Gly	Gly	Leu	Gly	Ser	Leu	Phe	Tyr	Leu	Thr	Leu		
				75					80					85			
gat	gtg	cta	gag	act	gac	tgc	cat	gtg	ctc	aga	aag	aag	gca	tgg	caa	342	
Asp	Val	Leu	Glu	Thr	Asp	Cys	His	Val	Leu	Arg	Lys	Lys	Ala	Trp	Gln		
			90					95					100				
gac	tgt	gga	atg	agg	ata	ttt	ttt	gaa	tca	gtt	tat	ggg	caa	tgc	aaa	390	
Asp	Cys	Gly	Met	Arg	Ile	Phe	Phe	Glu	Ser	Val	Tyr	Gly	Gln	Cys	Lys		
		105					110					115					
gca	ata	ttt	tat	atg	aac	aac	cca	agt	aga	gtt	ctc	tat	tta	gct	gct	438	
Ala	Ile	Phe	Tyr	Met	Asn	Asn	Pro	Ser	Arg	Val	Leu	Tyr	Leu	Ala	Ala		
	120					125					130						
tat	aac	tgt	act	ctt	cgc	cca	gtt	tca	aaa	aaa	aag	att	tac	atg	acg	486	
Tyr	Asn	Cys	Thr	Leu	Arg	Pro	Val	Ser	Lys	Lys	Lys	Ile	Tyr	Met	Thr		
135					140					145					150		
tgc	cct	gac	tgc	cca	agc	tcc	ata	ccc	act	gac	tct	tcc	aac	cac	caa	534	
Cys	Pro	Asp	Cys	Pro	Ser	Ser	Ile	Pro	Thr	Asp	Ser	Ser	Asn	His	Gln		
				155					160					165			
gtg	ctg	gag	gct	gcc	acc	gag	tct	ctt	gcg	aaa	tac	aac	aac	gag	aac	582	
Val	Leu	Glu	Ala	Ala	Thr	Glu	Ser	Leu	Ala	Lys	Tyr	Asn	Asn	Glu	Asn		
			170					175					180				
aca	tcc	aag	cag	tat	tct	ctc	ttc	aaa	gtc	acc	agg	gct	tct	agc	cag	630	
Thr	Ser	Lys	Gln	Tyr	Ser	Leu	Phe	Lys	Val	Thr	Arg	Ala	Ser	Ser	Gln		
		185					190					195					
tgg	gtg	gtc	ggc	cct	tct	tac	ttt	gtg	gaa	tac	tta	att	aaa	gaa	tca	678	
Trp	Val	Val	Gly	Pro	Ser	Tyr	Phe	Val	Glu	Tyr	Leu	Ile	Lys	Glu	Ser		
	200					205					210						
cca	tgt	act	aaa	tcc	cag	gcc	agc	agc	tgt	tca	ctt	cag	tcc	tcc	gac	726	
Pro	Cys	Thr	Lys	Ser	Gln	Ala	Ser	Ser	Cys	Ser	Leu	Gln	Ser	Ser	Asp		
215					220				225						230		
tct	gtg	cct	gtt	ggg	ctt	tgc	aaa	ggg	tct	ctg	act	cga	aca	cac	tgg	774	
Ser	Val	Pro	Val	Gly	Leu	Cys	Lys	Gly	Ser	Leu	Thr	Arg	Thr	His	Trp		
				235					240					245			
gaa	aag	ttt	gtc	tct	gtg	act	tgt	gac	ttc	ttt	gaa	tca	cag	gct	cca	822	
Glu	Lys	Phe	Val	Ser	Val	Thr	Cys	Asp	Phe	Phe	Glu	Ser	Gln	Ala	Pro		
			250					255					260				
gcc	act	gga	agt	gaa	aac	tct	gct	gtt	aac	cag	aaa	cct	aca	aac	ctt	870	
Ala	Thr	Gly	Ser	Glu	Asn	Ser	Ala	Val	Asn	Gln	Lys	Pro	Thr	Asn	Leu		
		265					270					275					
ccc	aag	gtg	gaa	gaa	tcc	cag	cag	aaa	aac	acc	ccc	cca	aca	gac	tcc	918	
Pro	Lys	Val	Glu	Glu	Ser	Gln	Gln	Lys	Asn	Thr	Pro	Pro	Thr	Asp	Ser		
	280					285					290						
ccc	tcc	aaa	gct	ggg	cca	aga	gga	tct	gtc	caa	tat	ctt	cct	gac	ttg	966	
Pro	Ser	Lys	Ala	Gly	Pro	Arg	Gly	Ser	Val	Gln	Tyr	Leu	Pro	Asp	Leu		
295					300				305						310		
gat	gat	aaa	aat	tcc	cag	gaa	aag	ggc	cct	cag	gag	gcc	ttt	cct	gtg	1014	
Asp	Asp	Lys	Asn	Ser	Gln	Glu	Lys	Gly	Pro	Gln	Glu	Ala	Phe	Pro	Val		

315	320	325	
cat ctg gac cta acc acg aat ccc cag gga gaa acc ctg gat att tcc			1062
His Leu Asp Leu Thr Thr Asn Pro Gln Gly Glu Thr Leu Asp Ile Ser			
330	335	340	
ttc ctc ttc ctg gag cct atg gag gag aag ctg gtt gtc ctg cct ttc			1110
Phe Leu Phe Leu Glu Pro Met Glu Glu Lys Leu Val Val Leu Pro Phe			
345	350	355	
ccc aaa gaa aaa gca cgc act gct gag tgc cca ggg cca gcc cag aat			1158
Pro Lys Glu Lys Ala Arg Thr Ala Glu Cys Pro Gly Pro Ala Gln Asn			
360	365	370	
gcc agc cct ctt gtc ctt ccg cca tga gaatcacaca gagtcttctg			1205
Ala Ser Pro Leu Val Leu Pro Pro *			
375	380		
taggggtatg gtgcgccgca tgacatggga ggcatgggg acgatggaca gagacagagc			1265
gtgcacacgt agagtggcta gtgaaggacg cctttttgac tcttcttggt ctcagcatgt			1325
tgactgggat tggaaataat gagactgagc cctcggtctg ggctgcactc taccctgtac			1385
actgccttgt accctgagct gcatcacctc ctaaactgag cagtctcata ccatggagag			1445
atgcctctct tatgtcttca gccactcact tataaagata cttatctttt cagcagt			1502
<210> 38			
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<220>			
<221> CDS			
<222> (111)...(1064)			
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tctaggactg gactcttcct aagcaagtcc gagaaggaag caccctcact atg tgg			116
		Met Trp	
		1	
ctc tac ctg gcg gcc ttc gtg ggc ctg tac tac ctt ctg cac tgg tac			164
Leu Tyr Leu Ala Ala Phe Val Gly Leu Tyr Tyr Leu Leu His Trp Tyr			
5	10	15	
cgg gag agg cag gtg gtg agc cac ctc caa gac aag tat gtc ttt atc			212
Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val Phe Ile			
20	25	30	
acg ggc tgt gac tcg ggc ttt ggg aac ctg ctg gcc aga cag ctg gat			260
Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln Leu Asp			
35	40	45	50
gca cga ggc ttg aga gtg ctg gct gcg tgt ctg acg gag aag ggg gcc			308
Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys Gly Ala			
55	60	65	
gag cag ctg agg ggc cag acg tct gac agg ctg gag acg gtg acc ctg			356
Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val Thr Leu			
70	75	80	
gat gtt acc aag atg gag agc atc gct gca gct act cag tgg gtg aag			404
Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp Val Lys			

21

gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc tac cag 627
Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln
190 195 200

gag ctg acc cag ctg aag gct gca gtg ggt gag ttg cca gac cag tcc 675
Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser
205 210 215

aag cag cag caa atc tat caa gaa ctg acc gat ttg aag act gca ttt 723
Lys Gln Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe
220 225 230

gaa cgc ctg tgc cgc cac tgt ccc aag gac tgg aca ttc ttc caa gga 771
Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly
235 240 245

aac tgt tac ttc atg tct aac tcc cag cgg aac tgg cac gac tcc gtc 819
Asn Cys Tyr Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser Val
250 255 260 265

acc gcc tgc cag gaa gtg agg gcc cag ctc gtc gta atc aaa act gct 867
Thr Ala Cys Gln Glu Val Arg Ala Gln Leu Val Val Ile Lys Thr Ala
270 275 280

gag gag cag ctt cca gcg gta ctg gaa cag tgg aga acc caa caa tag 915
Glu Glu Gln Leu Pro Ala Val Leu Glu Gln Trp Arg Thr Gln Gln *
285 290 295

cggggaatgaa gactgtgcgg aatttagtgg cagtggctgg aacgacaatc gatgtgacgt 975
tgacaattac tggatctgca aaaagccgc agcctgcttc agagacgaat agttgtttcc 1035
ctgctagcct cagcctccat tgtggtatag cagaacttca cccacttgta agccagcgct 1095
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atccccatg aacctgggtc ttattctgtc cttctgatgc ctccaagttt cctgggtgta 1215
gagcttgtgt tcttggccca tccttggagc tttataagtg acctgagtgg gatgcattta 1275
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gagctcatct tgcaggctgg aagcaccagg gaattaattc cccagtcaa ccaatggcat 1515
ccagagaggg catggaggct ccatacaacc tcttccaccc ccacatcttt ctttgtccta 1575
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gtaactgc 1643

<210> 40
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (38)...(631)

<400> 40
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Met Cys Thr Gly Lys Cys
1 5

gcc cgc tgt gtg ggg ctc tcc ctc att acc ctc tgc ctc gtc tgc att 103
Ala Arg Cys Val Gly Leu Ser Leu Ile Thr Leu Cys Leu Val Cys Ile
10 15 20

gtg gcc aac gcc ctc ctg ctg gta cct aat ggg gag acc tcc tgg acc 151

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Val Ala Asn Ala Leu Leu Leu Val Pro Asn Gly Glu Thr Ser Trp Thr
      25                      30                      35

aac acc aac cat ctc agc ttg caa gtc tgg ctc atg ggc ggc ttc att 199
Asn Thr Asn His Leu Ser Leu Gln Val Trp Leu Met Gly Gly Phe Ile
      40                      45                      50

ggc ggg ggc cta atg gta ctg tgt ccg ggg att gca gcc gtt cgg gca 247
Gly Gly Gly Leu Met Val Leu Cys Pro Gly Ile Ala Ala Val Arg Ala
      55                      60                      65

ggg ggc aag ggc tgc tgt ggt gct ggg tgc tgt gga aac cgc tgc agg 295
Gly Gly Lys Gly Cys Cys Gly Ala Gly Cys Cys Gly Asn Arg Cys Arg
      75                      80                      85

atg ctg cgc tcg gtc ttc tcc tcg gcg ttc ggg gtg ctt ggt gcc atc 343
Met Leu Arg Ser Val Phe Ser Ser Ala Phe Gly Val Leu Gly Ala Ile
      90                      95                      100

tac tgc ctc tcg gtg tct gga gct ggg ctc cga aat gga ccc aga tgc 391
Tyr Cys Leu Ser Val Ser Gly Ala Gly Leu Arg Asn Gly Pro Arg Cys
      105                      110                      115

tta atg aac ggc gag tgg ggc tac cac ttc gaa gac acc gcg gga gct 439
Leu Met Asn Gly Glu Trp Gly Tyr His Phe Glu Asp Thr Ala Gly Ala
      120                      125                      130

tac ttg ctc aac cgc act cta tgg gat ccg tgc gag gcg ccc cct cgc 487
Tyr Leu Leu Asn Arg Thr Leu Trp Asp Arg Cys Glu Ala Pro Pro Arg
      135                      140                      145                      150

gtg gtc ccc tgg aat gtg acg ctc ttc tcg ctg ctg gtg gcc gcc tcc 535
Val Val Pro Trp Asn Val Thr Leu Phe Ser Leu Leu Val Ala Ala Ser
      155                      160                      165

tgc ctg gag ata gta ctg tgt ggg atc cag ctg gtg aac gcg acc att 583
Cys Leu Glu Ile Val Leu Cys Gly Ile Gln Leu Val Asn Ala Thr Ile
      170                      175                      180

ggt gtc ttc tgc ggc gat tgc agg aaa aaa cag gac acc cct cac tga 631
Gly Val Phe Cys Gly Asp Cys Arg Lys Lys Gln Asp Thr Pro His *
      185                      190                      195

ggctccactg accgccgggt tacacctget ccttccctgga cgccctacctg gctcgcctcac 691
tcccttgctc gctagaataa actgctttgc gctctctt 729

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<210> 41
 <211> 1322
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (84)...(749)

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<400> 41
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cgcggggatcc gactctagtc gta atg gag gcg ggc ggc ttt ctg gac tcg ctc 113
      Met Glu Ala Gly Gly Phe Leu Asp Ser Leu
              1                      5                      10

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att tac gga gca tgc gtg gtc ttc acc ctt ggc atg ttc tcc gcc ggc	161
Ile Tyr Gly Ala Cys Val Val Phe Thr Leu Gly Met Phe Ser Ala Gly	
15 20 25	
ctc tcg gac ctc agg cac atg cga atg acc cgg agt gtg gac aac gtc	209
Leu Ser Asp Leu Arg His Met Arg Met Thr Arg Ser Val Asp Asn Val	
30 35 40	
cag ttc ctg ccc ttt ctc acc acg gaa gtc aac aac ctg ggc tgg ctg	257
Gln Phe Leu Pro Phe Leu Thr Thr Glu Val Asn Asn Leu Gly Trp Leu	
45 50 55	
agt tat ggg gct ttg aag gga gac ggg atc ctc atc gtc gtc aac aca	305
Ser Tyr Gly Ala Leu Lys Gly Asp Gly Ile Leu Ile Val Val Asn Thr	
60 65 70	
gtg ggt gct gcg ctt cag acc ctg tat atc ttg gca tat ctg cat tac	353
Val Gly Ala Ala Leu Gln Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr	
75 80 85 90	
tgc cct cgg aag cgt gtt gtg ctc cta cag act gca acc ctg cta ggc	401
Cys Pro Arg Lys Arg Val Val Leu Leu Gln Thr Ala Thr Leu Leu Gly	
95 100 105	
gtc ctt ctc ctg ggt tat ggc tac ttt tgg ctc ctg gta ccc aac cct	449
Val Leu Leu Leu Gly Tyr Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro	
110 115 120	
gag gcc cgg ctt cag cag ttg ggc ctc ttc tgc agt gtc ttc acc atc	497
Glu Ala Arg Leu Gln Gln Leu Gly Leu Phe Cys Ser Val Phe Thr Ile	
125 130 135	
agc atg tac ctc tca cca ctg gct gac ttg gct aag gtg att caa act	545
Ser Met Tyr Leu Ser Pro Leu Ala Asp Leu Ala Lys Val Ile Gln Thr	
140 145 150	
aaa tca acc caa tgt ctc tcc tac cca ctc acc att gct acc ctt ctc	593
Lys Ser Thr Gln Cys Leu Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu	
155 160 165 170	
acc tct gcc tcc tgg tgc ctc tat ggg ttt cga ctc aga gat ccc tat	641
Thr Ser Ala Ser Trp Cys Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr	
175 180 185	
atc atg gtg tcc aac ttt cca gga atc gtc acc agc ttt atc cgc ttc	689
Ile Met Val Ser Asn Phe Pro Gly Ile Val Thr Ser Phe Ile Arg Phe	
190 195 200	
tgg ctt ttc tgg aag tac ccc cag gag caa gac agg aac tac tgg ctc	737
Trp Leu Phe Trp Lys Tyr Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu	
205 210 215	
ctg caa acc tga ggctgctcat ctgaccactg ggcaccttag tgccaacctg	789
Leu Gln Thr *	
220	
aaccaaagag acctccttgt ttcagctggg cctgctgtcc agcttcccag gtgcagtgagg	849
ttgtgggaac aagagatgac tttgaggata aaaggaccaa agaaaaagct ttacttagat	909
gattgattgg ggcctaggag atgaaatcac tttttatattt ttagagattt ttttttttaa	969
ttttggagggt tggggtgcaa tcttttagaat atgccttaaaa aggccgggag cggtgggtca	1029
cgctgtgaat cccagcactt tgggaggcca aggtgggagc atcgctgag gtcaggagtt	1089

caagaccaac ctgactaaca tgggtgaaacc ccatctctac taaaaataca aaattagcca 1149
 ggcattgatgg cacatgcctg taatcccaga tactttgggag gctgaggcag gagaattgct 1209
 tgaacccagg aggtggaggt tgcagtgagc tgagatcgtg ccattgtgat atgaatatgc 1269
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<210> 42
 <211> 3045
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (191)...(946)

<400> 42
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 ccgccttctg catcgcggtt tcggcggtt ccacctagac acctaacagt cgcggagccg 120
 gccgcgtcgt gagggggtcg gcacggggag tcgggcggtc ttgtgcatct tggctacctg 180
 tgggtcgaag atg tcg gac atc gga gac tgg ttc agg agc atc ccg gcg 229
 Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala
 1 5 10

atc acg cgc tat tgg ttc gcc gcc acc gtc gcc gtg ccc ttg gtc ggc 277
 Ile Thr Arg Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly
 15 20 25

aaa ctc ggc ctc atc agc ccg gcc tac ctc ttc ctc tgg ccc gaa gcc 325
 Lys Leu Gly Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala
 30 35 40 45

ttc ctt tat cgc ttt cag att tgg agg cca atc act gcc acc ttt tat 373
 Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr
 50 55 60

ttc cct gtg ggt cca gga act gga ttt ctt tat ttg gtc aat tta tat 421
 Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr
 65 70 75

ttc tta tat cag tat tct acg cga ctt gaa aca gga gct ttt gat ggg 469
 Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly
 80 85 90

agg cca gca gac tat tta ttc atg ctc ctc ttt aac tgg att tgc atc 517
 Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile
 95 100 105

gtg att act ggc tta gca atg gat atg cag ttg ctg atg att cct ctg 565
 Val Ile Thr Gly Leu Ala Met Asp Met Gln Leu Leu Met Ile Pro Leu
 110 115 120 125

atc atg tca cta ctt tat gtc tgg gcc cag ctg aac aga gac atg att 613
 Ile Met Ser Leu Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile
 130 135 140

gta tca ttt tgg ttt gga aca cga ttt aag gcc tgc tat tta ccc tgg 661
 Val Ser Phe Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp
 145 150 155

gtt atc ctt gga ttc aac tat atc atc gga ggc tcg gta atc aat gag 709
 Val Ile Leu Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu
 160 165 170

ctt att gga aat ctg gtt gga cat ctt tat ttt ttc cta atg ttc aga 757
 Leu Ile Gly Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg
 175 180 185

tac cca atg gac ttg gga gga aga aat ttt cta tcc aca cct cag ttt 805
 Tyr Pro Met Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe
 190 195 200 205

ttg tac cgc tgg ctg ccc agt agg aga gga gga gta tca gga ttt ggt 853
 Leu Tyr Arg Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly
 210 215 220

gtg ccc cct gct agc atg agg cga gct gct gat cag aat ggc gga ggc 901
 Val Pro Pro Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly
 225 230 235

ggg aga cac aac tgg ggc cag ggc ttt cga ctt gga gac cag tga 946
 Gly Arg His Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln *
 240 245 250

agggggcggcc tcgggcagcc gctcctctca agccacattt cctcccagtg ctgggtgcgc 1006
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 gtacgagaca aagtttctta aatcccgaag aaaaatataa gtgttccaca agtttcacga 1126
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 cccgtttttt ggtcatgttt caattaattg tgaggaaggc gcagctcctc tctgcacgta 2026
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 agttattcct cttaaacatg gtttaggaagc tgatgacgtt attgattttg tctggattat 2866
 gtttctggaa taattttacc aaaacaagct atttgagttt tgacttgaca aggcaaaaca 2926
 tgacagtgga ttctctttac aaattgaaaa aaataatcct tattttgtat aaaggacttc 2986
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 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (63)...(383)

<400> 43

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ac atg gcg act ccc ggc cct gtg att ccg gag gtc ccc ttt gaa cca 107
Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro
1 5 10 15

tcg aag cct cca gtc att gag ggg ctg agc ccc act gtt tac agg aat 155
Ser Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn
20 25 30

cca gag agt ttc aag gaa aag ttc gtt cgc aag acc cgc gag aac ccg 203
Pro Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro
35 40 45

gtg gta ccc ata ggt tgc ctg gcc acg gcg gcc gcc ctc acc tac ggc 251
Val Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Ala Leu Thr Tyr Gly
50 55 60

ctc tac tcc ttc cac cgg ggc aac agc cag cgc tct cag ctc atg atg 299
Leu Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met
65 70 75

cgc acc cgg atc gcc gcc cag ggt ttc acg gtc gca gcc atc ttg ctg 347
Arg Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu
80 85 90 95

ggc ctg gct gtc act gct atg aag tct cga ccc taa gccagggtc 393
Gly Leu Ala Val Thr Ala Met Lys Ser Arg Pro *
100 105

tggccttgaa agctccgcag aaatgattcc aaaacccagg gagcaaccac tggccctacc 453
gtgggactta ctccctctc tcctttgaga ggcccatgtg tcgctgggga ggaagtgacc 513
ctttgtgtaa ctgtaaccga aagttttttc aaaaatccta gatgctgttg tttgaatgtt 573
acatacttct atttgtgccat catctcccct ccaactcccct gcttaataaa ctctaaaaat 633
ccacttgtat ttaattcagt 653

<210> 44

<211> 439

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)...(311)

<400> 44

gtagaaacag gcctgttaag gagaggccac cgggacttca gtgtctctc catcccagga 60
gcgcagtggc cact atg ggg tct ggg ctg ccc ctt gtc ctc ctc ttg acc 110
Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr
1 5 10

ctc ctt ggc agc tca cat gga aca ggg ccg ggt atg act ttg caa ctg 158
Leu Leu Gly Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu
15 20 25

aag ctg aag gag tct ttt ctg aca aat tcc tcc tat gag tcc agc ttc 206

```

Lys Leu Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe
  30                               35                               40

ctg gaa ttg ctt gaa aag ctc tgc ctc ctc ctc cat ctc cct tca ggg 254
Leu Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly
  45                               50                               55                               60

acc agc gtc acc ctc cac cat gca aga tct caa cac cat gtt gtc tgc 302
Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val Cys
                               65                               70                               75

aac aca tga cagccattga agcctgtgtc cttcttggcc cgggcttttg 351
Asn Thr *

ggccgggggat gcaggaggca ggccccgacc ctgtcttttca gcaggccccc accctcctga 411
gtggcaataa ataaaattcg gtatgctg 439

<210> 45
<211> 1131
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (56)...(1000)

<400> 45
ctatgagatc ccggcctcag ggtggacgca gtggtttctgc actgaggccc tcgtc atg 58
                                         Met
                                         1

gtg gcg cct gtg tgg tac ttg gta gcg gcg gct ctg cta gtc ggc ttt 106
Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly Phe
      5                               10                               15

atc ctc ttc ctg act cgc agc cgg ggc cgg gcg gca tca gcc ggc caa 154
Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly Gln
      20                               25                               30

gag cca ctg cac aat gag gag ctg gca gga gca ggc cgg gtg gcc cag 202
Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala Gln
      35                               40                               45

cct ggg ccc ctg gag cct gag gag ccg aga gct gga ggc agg cct cgg 250
Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro Arg
      50                               55                               60                               65

cgc cgg agg gac ctg ggc agc cgc cta cag gcc cag cgt cga gcc cag 298
Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala Gln
      70                               75                               80

cgg gtg gcc tgg gca gaa gca gat gag aac gag gag gaa gct gtc atc 346
Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val Ile
      85                               90                               95

cta gcc cag gag gag gaa ggt gtc gag aag cca gcg gaa act cac ctg 394
Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His Leu
      100                               105                               110

tcg ggg aaa att gga gct aag aaa ctg cgg aag ctg gag gag aaa caa 442

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Ser	Gly	Lys	Ile	Gly	Ala	Lys	Lys	Leu	Arg	Lys	Leu	Glu	Glu	Lys	Gln		
115						120					125						
gcg	cga	aag	gcc	cag	cgt	gag	gca	gag	gag	gct	gaa	cgt	gag	gag	cgg	490	
Ala	Arg	Lys	Ala	Gln	Arg	Glu	Ala	Glu	Glu	Ala	Glu	Arg	Glu	Glu	Arg		
130					135					140					145		
aaa	cga	ctc	gag	tcc	cag	cgc	gaa	gct	gag	tgg	aag	aag	gag	gag	gag	538	
Lys	Arg	Leu	Glu	Ser	Gln	Arg	Glu	Ala	Glu	Trp	Lys	Lys	Glu	Glu	Glu		
				150					155					160			
cgg	ctt	cgc	ctg	gag	gag	gag	cag	aag	gag	gag	gag	gag	agg	aag	gcc	586	
Arg	Leu	Arg	Leu	Glu	Glu	Glu	Gln	Lys	Glu	Glu	Glu	Glu	Arg	Lys	Ala		
				165				170					175				
cgc	gag	gag	cag	gcc	cag	cgg	gag	cat	gag	gag	tac	ctg	aaa	ctg	aag	634	
Arg	Glu	Glu	Gln	Ala	Gln	Arg	Glu	His	Glu	Glu	Tyr	Leu	Lys	Leu	Lys		
				180			185					190					
gag	gcc	ttt	gtg	gtg	gag	gag	gaa	ggc	gta	gga	gag	acc	atg	act	gag	682	
Glu	Ala	Phe	Val	Val	Glu	Glu	Glu	Gly	Val	Gly	Glu	Thr	Met	Thr	Glu		
	195					200					205						
gaa	cag	tcc	cag	agc	ttc	ctg	aca	gag	ttc	atc	aac	tac	atc	aag	cag	730	
Glu	Gln	Ser	Gln	Ser	Phe	Leu	Thr	Glu	Phe	Ile	Asn	Tyr	Ile	Lys	Gln		
210					215					220					225		
tcc	aag	gtt	gtg	ctc	ttg	gaa	gac	ctg	gct	tcc	cag	gtg	ggc	cta	cgc	778	
Ser	Lys	Val	Val	Leu	Leu	Glu	Asp	Leu	Ala	Ser	Gln	Val	Gly	Leu	Arg		
				230				235						240			
act	cag	gac	acc	ata	aat	cgc	atc	cag	gac	ctg	ctg	gct	gag	ggg	act	826	
Thr	Gln	Asp	Thr	Ile	Asn	Arg	Ile	Gln	Asp	Leu	Leu	Ala	Glu	Gly	Thr		
			245					250					255				
ata	aca	ggt	gtg	att	gac	gac	cgg	ggc	aag	ttc	atc	tac	ata	acc	cca	874	
Ile	Thr	Gly	Val	Ile	Asp	Asp	Arg	Gly	Lys	Phe	Ile	Tyr	Ile	Thr	Pro		
		260				265						270					
gag	gaa	ctg	gcc	gcc	gtg	gcc	aac	ttc	atc	cga	cag	cgg	ggc	cgg	gtg	922	
Glu	Glu	Leu	Ala	Ala	Val	Ala	Asn	Phe	Ile	Arg	Gln	Arg	Gly	Arg	Val		
	275					280					285						
tcc	atc	gcc	gag	ctt	gcc	caa	gcc	agc	aac	tcc	ctc	atc	gcc	tgg	ggc	970	
Ser	Ile	Ala	Glu	Leu	Ala	Gln	Ala	Ser	Asn	Ser	Leu	Ile	Ala	Trp	Gly		
290					295				300					305			
cgg	gag	tcc	cct	gcc	caa	gcc	cca	gcc	tga	ccccagtcct	tcctcttgg					1020	
Arg	Glu	Ser	Pro	Ala	Gln	Ala	Pro	Ala	*								
				310													
actcagagtt	ggtgtggcct	acctggctat	acatcttcat	ccctcccccac	catcctgggg											1080	
aagtgatggt	gtggccaggc	agttatagat	taaaggcctg	tgagtactgc	t											1131	

<210> 46
 <211> 1875
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (79)...(666)

<400> 46

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ctcgctcgct cagagggagg agaaagtggc gagttccgga tccctgccta gcgcggccca 60
acctttactc cagagatc atg gct gcc gag gat gtg gtg gcg act ggc gcc 111
          Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala
                1                5                10

gac cca agc gat ctg gag agc ggc ggg ctg ctg cat gag att ttc acg 159
Asp Pro Ser Asp Leu Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr
                15                20                25

tcg ccg ctc aac ctg ctg ctg ctt ggc ctc tgc atc ttc ctg ctc tac 207
Ser Pro Leu Asn Leu Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr
                30                35                40

aag atc gtg cgc ggg gac cag ccg gcg gcc agc ggc gac agc gac gac 255
Lys Ile Val Arg Gly Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp
                45                50                55

gac gag ccg ccc cct ctg ccc cgc ctc aag ccg cgc gac ttc acc ccc 303
Asp Glu Pro Pro Pro Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro
        60                65                70                75

gcc gag ctg ccg cgc ttc gac ggc gtc cag gac ccg cgc ata ctc atg 351
Ala Glu Leu Arg Arg Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met
                80                85                90

gcc atc aac ggc aag gtg ttc gat gtg acc aaa ggc cgc aaa ttc tac 399
Ala Ile Asn Gly Lys Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr
                95                100                105

ggg ccc gag ggg ccg tat ggg gtc ttt gct gga aga gat gca tcc agg 447
Gly Pro Glu Gly Pro Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg
                110                115                120

ggc ctt gcc aca ttt tgc ctg gat aag gaa gca ctg aag gat gag tac 495
Gly Leu Ala Thr Phe Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr
                125                130                135

gat gac ctt tct gac ctc act gct gcc cag cag gag act ctg agt gac 543
Asp Asp Leu Ser Asp Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp
        140                145                150                155

tgg gag tct cag ttc act ttc aag tat cat cac gtg ggc aaa ctg ctg 591
Trp Glu Ser Gln Phe Thr Phe Lys Tyr His His Val Gly Lys Leu Leu
                160                165                170

aag gag ggg gag gag ccc act gtg tac tca gat gag gaa gaa cca aaa 639
Lys Glu Gly Glu Glu Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys
                175                180                185

gat gag agt gcc ccg aaa aat gat taa agcattcagt ggaagtatat 686
Asp Glu Ser Ala Arg Lys Asn Asp *
                190                195

ctatTTTTgt attttgcaaa atcatttgta acagtccact ctgtcttttaa aacatagtga 746
ttacaatatt tagaaagttt tgagcacttg ctataagttt tttataacat cactagtgac 806
actaataaaa ttaacttctt agaatgcatg atgtgtttgt gtgtcacaaa tccagaaagt 866
gaactgcagt gctgtaatac acatgttaat actgtttttc ttctatctgt agttagtaca 926
ggatgaattt aaatgtgttt ttcttgagag acaaggaaga cttgggtatt tcccaaaaca 986

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ggtaaaaatc ttaaatgtgc accaagagca aaggatcaac ttttagtcat gatgttctgt 1046
aaagacaaca aatccctttt tttttctcaa ttgacttaac tgcattgatt ctgttttatac 1106
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ggttaaatag tcattgtatt ttcttgtgaa ctgtgtttta tgattttacc tcaaatcaga 1826
aaacaaaatg atgtgctttg gtcagttaat aaaaatgggt ttaccact 1875

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<210> 47

<211> 1562

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72)...(1460)

<400> 47

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aaattgggcc aggctgaggc gctgctgctg gagcggccga tccgagacgt ggctccctgg 60
gcggcagaac c atg ttg gac ttc gcg atc ttc gcc gtt acc ttc ttg ctg 110
          Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu
                1                5                10

```

```

gcg ttg gtg gga gcc gtg ctc tac ctc tat ccg gct tcc aga caa gct 158
Ala Leu Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala
    15                20                25

```

```

gca gga att cca ggg att act cca act gaa gaa aaa gat ggt aat ctt 206
Ala Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
    30                35                40                45

```

```

cca gat att gtg aat agt gga agt ttg cat gag ttc ctg gtt aat ttg 254
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn Leu
                50                55                60

```

```

cat gag aga tat ggg cct gtg gtc tcc ttc tgg ttt ggc agg cgc ctc 302
His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu
    65                70                75

```

```

gtg gtt agt ttg ggc act gtt gat gta ctg aag cag cat atc aat ccc 350
Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His Ile Asn Pro
    80                85                90

```

```

aat aag aca ttg gac cct ttt gaa acc atg ctg aag tca tta tta agg 398
Asn Lys Thr Leu Asp Pro Phe Glu Thr Met Leu Lys Ser Leu Leu Arg
    95                100                105

```

```

tat caa tct ggt ggt ggc agt gtg agt gaa aac cac atg agg aaa aaa 446
Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn His Met Arg Lys Lys
110                115                120                125

```

```

ttg tat gaa aat ggt gtg act gat tct ctg aag agt aac ttt gcc ctc 494
Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu Lys Ser Asn Phe Ala Leu

```


130										135										140									
ctc	cta	aag	ctt	tca	gaa	gaa	tta	tta	gat	aaa	tgg	ctc	tcc	tac	cca					542									
Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu	Asp	Lys	Trp	Leu	Ser	Tyr	Pro														
			145					150					155																
gag	acc	cag	cac	gtg	ccc	ctc	agc	cag	cat	atg	ctt	ggg	ttt	gct	atg					590									
Glu	Thr	Gln	His	Val	Pro	Leu	Ser	Gln	His	Met	Leu	Gly	Phe	Ala	Met														
		160					165					170																	
aag	tct	gtt	aca	cag	atg	gta	atg	ggg	agt	aca	ttt	gaa	gat	gat	cag					638									
Lys	Ser	Val	Thr	Gln	Met	Val	Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln														
		175				180					185																		
gaa	gtc	att	cgc	ttc	cag	aag	aat	cat	ggc	aca	gtt	tgg	tct	gag	att					686									
Glu	Val	Ile	Arg	Phe	Gln	Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile														
190					195				200						205														
gga	aaa	ggc	ttt	cta	gat	ggg	tca	ctt	gat	aaa	aac	atg	act	cgg	aaa					734									
Gly	Lys	Gly	Phe	Leu	Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys														
			210						215					220															
aaa	caa	tat	gaa	gat	gcc	ctc	atg	caa	ctg	gag	tct	gtt	tta	agg	aac					782									
Lys	Gln	Tyr	Glu	Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn														
			225					230					235																
atc	ata	aaa	gaa	cga	aaa	gga	agg	aac	ttc	agt	caa	cat	att	ttc	att					830									
Ile	Ile	Lys	Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile														
		240					245						250																
gac	tcc	tta	gta	caa	ggg	aac	ctt	aat	gac	caa	cag	atc	cta	gaa	gac					878									
Asp	Ser	Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp														
		255				260					265																		
agt	atg	ata	ttt	tct	ctg	gcc	agt	tgc	ata	ata	act	gca	aaa	ttg	tgt					926									
Ser	Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys														
270					275				280					285															
acc	tgg	gca	atc	tgt	ttt	tta	acc	acc	tct	gaa	gaa	gtt	caa	aaa	aaa					974									
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	Lys														
			290						295				300																
tta	tat	gaa	gag	ata	aac	caa	gtt	ttt	gga	aat	ggg	cct	gtt	act	cca					1022									
Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	Thr	Pro														
		305					310					315																	
gag	aaa	att	gag	cag	ctc	aga	tat	tgt	cag	cat	gtg	ctt	tgt	gaa	act					1070									
Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	Cys	Glu	Thr														
		320					325					330																	
gtt	cga	act	gcc	aaa	ctg	act	cca	gtt	tct	gcc	cag	ctt	caa	gat	att					1118									
Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	Leu	Gln	Asp	Ile														
		335				340					345																		
gaa	gga	aaa	att	gac	cga	ttt	att	att	cct	aga	gag	acc	ctc	gtc	ctt					1166									
Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	Glu	Thr	Leu	Val	Leu														
350					355				360					365															
tat	gcc	ctt	ggg	gtg	gta	ctt	cag	gat	cct	aat	act	tgg	cca	tct	cca					1214									
Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	Asn	Thr	Trp	Pro	Ser	Pro														
			370						375					380															

```

cac aag ttt gat cca gat cgg ttt gat gat gaa tta gta atg aaa act 1262
His Lys Phe Asp Pro Asp Arg Phe Asp Asp Glu Leu Val Met Lys Thr
                               385                               395

ttt tcc tca ctt gga ttc tca ggc aca cag gag tgt cca gag ttg agg 1310
Phe Ser Ser Leu Gly Phe Ser Gly Thr Gln Glu Cys Pro Glu Leu Arg
                               400                               410

ttt gca tat atg gtg acc aca gta ctt ctt agt gta ttg gtg aag aga 1358
Phe Ala Tyr Met Val Thr Thr Val Leu Leu Ser Val Leu Val Lys Arg
                               415                               425

ctg cac cta ctt tct gtg gag gga cag gtt att gaa aca aag tat gaa 1406
Leu His Leu Leu Ser Val Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu
430                               435                               440                               445

ctg gta aca tca tca agg gaa gaa gct tgg atc act gtc tca aag aga 1454
Leu Val Thr Ser Ser Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg
                               450                               455                               460

tat taa aattttatac atttaaaatc attgttaaatt tgattgagga aacaaccatt 1510
Tyr *

taaaaaaaaaat ctatgttgaa tcctttttata aaccagtatc acttttgaat at 1562

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<211> 2030
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (171)...(914)

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gcgccccctcg tggggtcgcg ttgccacccc acgcgggactc cccagctggc gcgccccctcc 120
catttgccctg tcctggtcag gccccacccc cccttcccac ctgaccagcc atg ggg 176
                                                Met Gly
                                                1

gct gcg gtg ttt ttc ggc tgc act ttc gtc gcg ttc ggc ccg gcc ttc 224
Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro Ala Phe
                               5                               10                               15

gcg ctt ttc ttg atc act gtg gct ggg gac ccg ctt cgc gtt atc atc 272
Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu Arg Val Ile Ile
                               20                               25                               30

ctg gtc gca ggg gca ttt ttc tgg ctg gtc tcc ctg ctc ctg gcc tct 320
Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu Ala Ser
35                               40                               45                               50

gtg gtc tgg ttc atc ttg gtc cat gtg acc gac ccg tca gat gcc cgg 368
Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp Ala Arg
                               55                               60                               65

ctc cag tac ggc ctc ctg att ttt ggt gct gct gtc tct gtc ctt cta 416
Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val Leu Leu

```

35

```
gccactggag gagtcagact accatgacat cgtaggggaag gaggggagat ttttttgtag 1904
tttttaattg ggggtgtgga ggggcgggga gggttttctat aaactgtatc attttctgct 1964
gaggggtggag tgtcccatcc ttttaaatcaa ggtgattgtg attttgacta ataaaaaaga 2024
atttgt 2030
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<210> 49
 <211> 493
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (98)...(439)

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aaagttttccc aaatccaggc ggctagaggc ccactgcttc ccaactacca gctgaggggg 60
tccgtcccgga gaaggagaa gaggccgaag aggaaac atg aac ttc tat tta ctc 115
Met Asn Phe Tyr Leu Leu
1 5
```

```
cta gcg agc agc att ctg tgt gcc ttg att gtc ttc tgg aaa tat cgc 163
Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile Val Phe Trp Lys Tyr Arg
10 15 20
```

```
cgc ttt cag aga aac act ggc gaa atg tca tca aat tca act gct ctt 211
Arg Phe Gln Arg Asn Thr Gly Glu Met Ser Ser Asn Ser Thr Ala Leu
25 30 35
```

```
gca cta gtg aga ccc tct tct tct ggg tta att aac agc aat aca gac 259
Ala Leu Val Arg Pro Ser Ser Ser Gly Leu Ile Asn Ser Asn Thr Asp
40 45 50
```

```
aac aat ctt gca gtc tac gac ctc tct cgg gat att tta aat aat ttc 307
Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg Asp Ile Leu Asn Asn Phe
55 60 65 70
```

```
cca cac tca ata gcc agg cag aag cga ata ttg gta aac ctc agt atg 355
Pro His Ser Ile Ala Arg Gln Lys Arg Ile Leu Val Asn Leu Ser Met
75 80 85
```

```
gtg gaa aac aag ctg gtt gaa ctg gaa cat act cta ctt agc aag ggt 403
Val Glu Asn Lys Leu Val Glu Leu Glu His Thr Leu Leu Ser Lys Gly
90 95 100
```

```
ttc aga ggt cca tca cct cac cgg aaa tcc acc taa aagcgtacag 449
Phe Arg Gly Pro Ser Pro His Arg Lys Ser Thr *
105 110
```

```
gatgtaatgc cagtgggtgga aatcattaaa gacactttga gtag 493
```

<210> 50
 <211> 2044
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (288)...(1385)

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agattccggc ctggagctcc cagggccgag cagaccttgg gacctgtgag cgctgcatcc 60
```

```

aattaacccat gggaagggtc agcaccagcc accagcccct taggtgagga ctctgcctgg 120
ggctctgctg atggttccga atcatggagc tgcagagagc tcctccagcc tggagacgtt 180
cttggtgaaa gctgtggtct aactccaccg gctcttcctg cacattgtat tcaagagggg 240
tgctgcccc cgctgactca ggagctccgg tgctgcagcc gccacga atg ggg agg 296
                                     Met Gly Arg
                                     1

tgg gcc ctc gat gtg gcc ttt ttg tgg aag gcg gtg ttg acc ctg ggg 344
Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu Thr Leu Gly
      5                                10                                15

ctg gtg ctt ctc tac tac tgc ttc tcc atc ggc atc acc ttc tac aac 392
Leu Val Leu Leu Tyr Tyr Cys Phe Ser Ile Gly Ile Thr Phe Tyr Asn
  20                                25                                30                                35

aag tgg ctg aca aag agc ttc cat ttc ccc ctc ttc atg acg atg ctg 440
Lys Trp Leu Thr Lys Ser Phe His Phe Pro Leu Phe Met Thr Met Leu
                        40                                45                                50

cac ctg gcc gtg atc ttc ctc ttc tcc gcc ctg tcc agg gcg ctg gtt 488
His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser Arg Ala Leu Val
      55                                60                                65

cag tgc tcc agc cac agg gcc cgt gtg gtg ctg agc tgg gcc gac tac 536
Gln Cys Ser Ser His Arg Ala Arg Val Val Leu Ser Trp Ala Asp Tyr
      70                                75                                80

ctc aga aga gtg gct ccc aca gct ctg gcg acg gcg ctt gac gtg ggc 584
Leu Arg Arg Val Ala Pro Thr Ala Leu Ala Thr Ala Leu Asp Val Gly
      85                                90                                95

ttg tcc aac tgg agc ttc ctg tat gtc acc gtc tcg ctg tac aca atg 632
Leu Ser Asn Trp Ser Phe Leu Tyr Val Thr Val Ser Leu Tyr Thr Met
  100                                105                                110                                115

acc aaa tcc tca gct gtc ctc ttc atc ttg atc ttc tct ctg atc ttc 680
Thr Lys Ser Ser Ala Val Leu Phe Ile Leu Ile Phe Ser Leu Ile Phe
                        120                                125                                130

aag ctg gag gag ctg cgc gcg gca ctg gtc ctg gtg gtc ctc ctc atc 728
Lys Leu Glu Glu Leu Arg Ala Ala Leu Val Leu Val Val Leu Leu Ile
      135                                140                                145

gcc ggg ggt ctc ttc atg ttc acc tac aag tcc aca cag ttc aac gtg 776
Ala Gly Gly Leu Phe Met Phe Thr Tyr Lys Ser Thr Gln Phe Asn Val
      150                                155                                160

gag ggc ttc gcc ttg gtg ctg ggg gcc tcg ttc atc ggt ggc att cgc 824
Glu Gly Phe Ala Leu Val Leu Gly Ala Ser Phe Ile Gly Gly Ile Arg
      165                                170                                175

tgg acc ctc acc cag atg ctc ctg cag aag gct gaa ctc ggc ctc cag 872
Trp Thr Leu Thr Gln Met Leu Leu Gln Lys Ala Glu Leu Gly Leu Gln
  180                                185                                190                                195

aat ccc atc gac acc atg ttc cac ctg cag cca ctc atg ttc ctg ggg 920
Asn Pro Ile Asp Thr Met Phe His Leu Gln Pro Leu Met Phe Leu Gly
      200                                205                                210

ctc ttc cct ctc ttt gct gta ttt gaa ggt ctc cat ttg tcc aca tct 968
Leu Phe Pro Leu Phe Ala Val Phe Glu Gly Leu His Leu Ser Thr Ser

```

215	220	225	
gag aaa atc ttc cgt ttc cag gac aca ggg ctg ctc ctg cgg gta ctt			1016
Glu Lys Ile Phe Arg Phe Gln Asp Thr Gly Leu Leu Leu Arg Val Leu			
230	235	240	
ggg agc ctc ttc ctt ggc ggg att ctc gcc ttt ggt ttg ggc ttc tct			1064
Gly Ser Leu Phe Leu Gly Gly Ile Leu Ala Phe Gly Leu Gly Phe Ser			
245	250	255	
gag ttc ctc ctg gtc tcc aga acc tcc agc ctc act ctc tcc att gcc			1112
Glu Phe Leu Leu Val Ser Arg Thr Ser Ser Leu Thr Leu Ser Ile Ala			
260	265	270	275
ggc att ttt aag gaa gtc tgc act ttg ctg ttg gca gct cat ctg ctg			1160
Gly Ile Phe Lys Glu Val Cys Thr Leu Leu Leu Ala Ala His Leu Leu			
280	285	290	
ggc gat cag atc agc ctc ctg aac tgg ctg ggc ttc gcc ctc tgc ctc			1208
Gly Asp Gln Ile Ser Leu Leu Asn Trp Leu Gly Phe Ala Leu Cys Leu			
295	300	305	
tcg gga ata tcc ctc cac gtt gcc ctc aaa gcc ctg cat tcc aga ggt			1256
Ser Gly Ile Ser Leu His Val Ala Leu Lys Ala Leu His Ser Arg Gly			
310	315	320	
gat ggt ggc ccc aag gcc ttg aag ggg ctg ggc tcc agc ccc gac ctg			1304
Asp Gly Gly Pro Lys Ala Leu Lys Gly Leu Gly Ser Ser Pro Asp Leu			
325	330	335	
gag ctg ctg ctc cgg agc agc cag cgg gag gaa ggt gac aat gag gag			1352
Glu Leu Leu Leu Arg Ser Ser Gln Arg Glu Glu Gly Asp Asn Glu Glu			
340	345	350	355
gag gag tac ttt gtg gcc cag ggg cag cag tga ccagccaggg caaatggctt			1405
Glu Glu Tyr Phe Val Ala Gln Gly Gln Gln *			
360	365		
agaagcaggc cactccccag cctgctgcca gcaactcactg tgctcaagcc gccagggctc			1465
atcatggtag ctgggagctg tggacgggag tcaccagggtg gtggggccaa gccagggact			1525
catgactttt gcccctccct tcagagcctg gtcacacaag gggcgagcac caggccagcc			1585
tgggactggc cagagctggg cccaagctgc gctggaatcg cagcaggaga ggggagtggg			1645
ctgtttcttc ccaccacttc ccaggctctg acagccgaga ctcatttcca aggcacagca			1705
gctttctaaa gggactgagt ttggactggg ttttggaact ccaggggctg gagcttcac			1765
acctgggcag tgtcttttct cagagagcag gtttctttat agtttggaat taaatggttc			1825
acgggtccact ggccgccttg tggtgctgga gacgtggggg caggagggg acagtgtggg			1885
cctggcctct cctttccttt ccctgcctgg agccttcttc aaatgtctgg tcttaagcca			1945
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tgcacctgct ggcaggaaat aaatgaatgt ttactgagt			2044
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<213> Homo sapiens			
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<222> (157)...(837)			
<400> 51			
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tccattttcta aataccagac ttcaaaagat aaggttcaaa agtggttataa gaagatattc	120
cttttttttgt cctagagaac ttatttttcct gtgaaa atg cct acc aca aag aag	174
Met Pro Thr Thr Lys Lys	
1 5	
aca ttg atg ttc tta tca agc ttt ttc acc agc ctt ggg tcc ttc att	222
Thr Leu Met Phe Leu Ser Ser Phe Phe Thr Ser Leu Gly Ser Phe Ile	
10 15 20	
gta att tgc tct att ctt ggg aca caa gca tgg atc acc agt aca att	270
Val Ile Cys Ser Ile Leu Gly Thr Gln Ala Trp Ile Thr Ser Thr Ile	
25 30 35	
gct gtt aga gac tct gct tca aat ggg agc att ttc atc act tac gga	318
Ala Val Arg Asp Ser Ala Ser Asn Gly Ser Ile Phe Ile Thr Tyr Gly	
40 45 50	
ctt ttt cgt ggg gag agt agt gaa gaa ttg agt cac gga ctt gca gaa	366
Leu Phe Arg Gly Glu Ser Ser Glu Glu Leu Ser His Gly Leu Ala Glu	
55 60 65 70	
cca aag aaa aag ttt gca gtt tta gag ata ctg aat aat tct tcc caa	414
Pro Lys Lys Lys Phe Ala Val Leu Glu Ile Leu Asn Asn Ser Ser Gln	
75 80 85	
aaa act ctg cat tcg gtg act atc ctg ttc ctg gtc ctg agt ttg atc	462
Lys Thr Leu His Ser Val Thr Ile Leu Phe Leu Val Leu Ser Leu Ile	
90 95 100	
acg tcg ctg ctg agc tct ggg ttt acc ttc tac aac agc atc agc aac	510
Thr Ser Leu Leu Ser Ser Gly Phe Thr Phe Tyr Asn Ser Ile Ser Asn	
105 110 115	
cct tac cag aca ttc ctg ggg ccg acg ggg gtg tac acc tgg aac ggg	558
Pro Tyr Gln Thr Phe Leu Gly Pro Thr Gly Val Tyr Thr Trp Asn Gly	
120 125 130	
ctc ggt gca tcc ttc gtt ttt gtg acc atg ata ctg ttt gtg gcg aac	606
Leu Gly Ala Ser Phe Val Phe Val Thr Met Ile Leu Phe Val Ala Asn	
135 140 145 150	
acg cag tcc aac caa ctc tcc gaa gag ttg ttc caa atg ctt tac ccg	654
Thr Gln Ser Asn Gln Leu Ser Glu Glu Leu Phe Gln Met Leu Tyr Pro	
155 160 165	
gca acc acc agt aaa gga acg acc cac agt tac gga tac tcg ttc tgg	702
Ala Thr Thr Ser Lys Gly Thr Thr His Ser Tyr Gly Tyr Ser Phe Trp	
170 175 180	
ctc ata ctg ctc gtc att ctt cta aat ata gtc act gta acc atc atc	750
Leu Ile Leu Leu Val Ile Leu Leu Asn Ile Val Thr Val Thr Ile Ile	
185 190 195	
att ttc tac cag aag gcc aga tac cag cgg aag cag gag cag aga aag	798
Ile Phe Tyr Gln Lys Ala Arg Tyr Gln Arg Lys Gln Glu Gln Arg Lys	
200 205 210	
cca atg gaa tat gct cca agg gac gga att tta ttc tga attctcttttc	847
Pro Met Glu Tyr Ala Pro Arg Asp Gly Ile Leu Phe *	
215 220 225	

```

atctcattttt ggcgttgcat ctattgtaca tcagccctga gtagtaactg gtttagcttct 907
ctggacaatt cagcatggta acgtgactgt catctgtgac agcattttgtg ttatcatgaca 967
ctgtgttctt cattgatgct gtactcctga aaatttttcc cacaagggtg gggaaatgaa 1027
tgggaaatgt cgctgg                                     1043

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<210> 52
 <211> 971
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (29)...(418)

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<400> 52
agacagcggc gggcgcagga cgtgcact atg gct cgg ggc tcg ctg cgc cgg      52
                               Met Ala Arg Gly Ser Leu Arg Arg
                               1           5

ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc      100
Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser
   10           15           20

gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc      148
Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser
   25           30           35           40

tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg      196
Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg
           45           50           55

gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct      244
Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro
           60           65           70

gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg      292
Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu
           75           80           85

acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc      340
Thr Phe Val Leu Gly Leu Ser Gly Phe Leu Val Trp Arg Arg Cys
           90           95          100

cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag      388
Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu
   105           110           115           120

ggc tgc cca gct gtg gcg ctg atc cag tga caatgtgcc cctgccaccg      438
Gly Cys Pro Ala Val Ala Leu Ile Gln *
           125

gggctcgccc actcatcatt cattcatcca ttctagagcc agtctctgcc tcccagacgc 498
ggcgggagcc aagctcctcc aaccacaagg ggggtggggg gcggtgaatc acctctgagg 558
cctgggcccc ggggttcaggg gaaccttcca aggtgtctgg ttgccctgcc tctggctcca 618
gaacagaaag ggagcctcac gctggctcac acaaaacagc tgacactgac taagggaactg 678
cagcattttg acaggggagg ggggtgccct ccttcctaga ggccctgggg gccaggctga 738
cttggggggc agacttgaca ctaggcccc ctcactcaga tgtcctgaaa ttccaccacg 798
ggggtcaccc tgggggggta gggacctatt tttaacacta gggggctggc ccactaggag 858
ggctggccct aagatacaga ccccccaac tccccaaagc ggggaggaga tattttatatt 918
ggggagagtt tggaggggag ggagaattta ttaataaaag aatctttaac ttt      971

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<210> 53
 <211> 695
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (73)...(564)

<400> 53
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 tgacacggaa gc atg cga cgg ctg ctg atc cct ctg gcc ctg tgg ctg ggc 111
 Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly
 1 5 10

gcg gtg ggc gtg ggc gtc gcc gag ctc acg gaa gcc cag cgc cgg ggc 159
 Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly
 15 20 25

ctg cag gtg gcc ctg gag gaa ttt cac aag cac ccg ccc gtg cag tgg 207
 Leu Gln Val Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp
 30 35 40 45

gcc ttc cag gag acc agt gtg gag agc gcc gtg gac acg ccc ttc cca 255
 Ala Phe Gln Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro
 50 55 60

gct gga ata ttt gtg agg ctg gaa ttt aag ctg cag cag aca agc tgc 303
 Ala Gly Ile Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys
 65 70 75

cgg aag agg gac tgg aag aaa ccc gag tgc aaa gtc agg ccc aat ggg 351
 Arg Lys Arg Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly
 80 85 90

agg aaa cgg aaa tgc ctg gcc tgc atc aaa ctg ggc tct gag gac aaa 399
 Arg Lys Arg Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys
 95 100 105

gtt ctg ggc cgg ttg gtc cac tgc ccc ata gag acc caa gtt ctg cgg 447
 Val Leu Gly Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg
 110 115 120 125

gag gct gag gag cac cag gag acc cag tgc ctc agg gtg cag cgg gct 495
 Glu Ala Glu Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala
 130 135 140

ggt gag gac ccc cac agc ttc tac ttc cct gga cag ttc gcc ttc tcc 543
 Gly Glu Asp Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser
 145 150 155

aag gcc ctg ccc cgc agc taa gccagcactg agctgcgtgg tgcctccagg 594
 Lys Ala Leu Pro Arg Ser *
 160

accgctgccg gtggtaacca gtggaagacc ccagccccca gggagaggac cccgttctat 654
 cccagccat gataataaag ctgctctccc agctgcctct c 695

<210> 54
 <211> 1914
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (80)...(661)

<400> 54

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actctctgct gtcgcccgtc ccgcgcgctc ctccgacccg ctccgctccg ctccgctcgg 60
ccccgcgccg cccgtcaac atg atc cgc tgc ggc ctg gcc tgc gag cgc tgc 112
          Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys
                1                5                10

cgc tgg atc ctg ccc ctg ctc cta ctc agc gcc atc gcc ttc gac atc 160
Arg Trp Ile Leu Pro Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile
          15                20                25

atc gcg ctg gcc ggc cgc ggc tgg ttg cag tct agc gac cac ggc cag 208
Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln
          30                35                40

acg tcc tcg ctg tgg tgg aaa tgc tcc caa gag ggc ggc ggc agc ggg 256
Thr Ser Ser Leu Trp Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly
          45                50                55

tcc tac gag gag ggc tgt cag agc ctc atg gag tac gcg tgg ggt aga 304
Ser Tyr Glu Glu Gly Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg
          60                65                70                75

gca gcg gct gcc atg ctc ttc tgt ggc ttc atc atc ctg gtg atc tgt 352
Ala Ala Ala Ala Met Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys
          80                85                90

ttc atc ctc tcc ttc ttc gcc ctc tgt gga ccc cag atg ctt gtc ttc 400
Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe
          95                100                105

ctg aga gtg att gga ggt ctc ctt gcc ttg gct gct gtg ttc cag atc 448
Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile
          110                115                120

atc tcc ctg gta att tac ccc gtg aag tac acc cag acc ttc acc ctt 496
Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu
          125                130                135

cat gcc aac cgt gct gtc act tac atc tat aac tgg gcc tac ggc ttt 544
His Ala Asn Arg Ala Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe
          140                145                150                155

ggg tgg gca gcc acg att atc ctg atc ggc tgt gcc ttc ttc ttc tgc 592
Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys
          160                165                170

tgc ctc ccc aac tac gaa gat gac ctt ctg ggc aat gcc aag ccc agg 640
Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg
          175                180                185

tac ttc tac aca tct gcc taa cttgggaatg aatgtgggag aaaatcgctg 691
Tyr Phe Tyr Thr Ser Ala *
          190

ctgctgagat ggactccaga agaagaaact gtttctccag gcgactttga acccattttt 751

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tggcagtgtt catattatta aactagtcaa ataagctaaa ataatttggg agaaaatatt 811
ttttaagtag tgttataagtt tcatgtttat cttttattat gttttgtgaa gttgtgtctt 871
ttcactaatt acctatacta tgccaatatt tccttatatc tatccataac atttatacta 931
catttgtaag agaatatgca cgtgaaactt aacactttat aaggtaaaaa tgagggttcc 991
aagatttaaat aatctgatca agttcttggt atttccaaat agaattggact tgggtctgta 1051
agggctaagg agaagaggaa gataagggtta aaagttgtta atgaccaaac attctaaaag 1111
aaatgcaaaa aaaaagttaa ttttcaagcc ttogaactat ttaaggaaag caaaatcatt 1171
tcctaaatgc atatcatttg tgagaatttc tcattaatat cctgaatcat tcatttcagc 1231
taaggcttca tgttgactcg atatgtcatc taggaaagta ctatttcatg gtccaaacct 1291
gttgccatag ttggtaaggc tttcctttaa gtgtgaaata tttagatgaa attttctctt 1351
ttaaagttct ttatagggtt aggggtgtggg aaaatgctat attaataaat ctgtagtggt 1411
ttgtgtttat atgttcagaa ccagagtaga ctggattgaa agatggactg ggtctaattt 1471
atcatgactg atagatctgg ttaagttgtg tagtaaagca ttaggagggt cattcttgtc 1531
acaaaagtgc cactaaaaca gcctcaggag aataaatgac ttgcttttct aaatctcagg 1591
tttatctggg ctctatcata tagacaggct tctgatagtt tgcaactgta agcagaaacc 1651
tacatatagt taaaatcctg gtctttcttg gtaaacagat tttaaatgtc tgatataaaa 1711
catgccacag gagaattcgg ggatttgagt ttctctgaat agcatatata tgatgcatcg 1771
gataggatcat tatgattttt taccatttcg acttacataa tgaaaaccaa ttcattttta 1831
atatcagatt attattttgt aagttgtgga aaaagctaatt ttagtgtttc attatgaagt 1891
tttcccaata aaccaggtat tct 1914

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<210> 55
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 55
 gatcccgggt cacgtgggat

20

<210> 56
 <211> 16
 <212> DNA
 <213> Homo sapiens

<400> 56
 atcccacgtg acccgg

16

<210> 57
 <211> 367
 <212> PRT
 <213> Homo sapiens

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<400> 57
Met Lys Ser Leu Val Leu Leu Leu Cys Leu Ala Gln Leu Trp Gly Cys
 1           5           10           15
His Ser Ala Pro His Gly Pro Gly Leu Ile Tyr Arg Gln Pro Asn Cys
 20           25           30
Asp Asp Pro Glu Thr Glu Glu Ala Ala Leu Val Ala Ile Asp Tyr Ile
 35           40           45
Asn Gln Asn Leu Pro Trp Gly Tyr Lys His Thr Leu Asn Gln Ile Asp
 50           55           60
Glu Val Lys Val Trp Pro Gln Gln Pro Ser Gly Glu Leu Phe Glu Ile
 65           70           75           80
Glu Ile Asp Thr Leu Glu Thr Thr Cys His Val Leu Asp Pro Thr Pro
 85           90           95
Val Ala Arg Cys Ser Val Arg Gln Leu Lys Glu His Ala Val Glu Gly
100          105          110
Asp Cys Asp Phe Gln Leu Leu Lys Leu Asp Gly Lys Phe Ser Val Val
115          120          125
Tyr Ala Lys Cys Asp Ser Ser Pro Asp Ser Ala Glu Asp Val Arg Lys
130          135          140

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Val Cys Gln Asp Cys Pro Leu Leu Ala Pro Leu Asn Asp Thr Arg Val
 145 150 155 160
 Val His Ala Ala Lys Ala Ala Leu Ala Ala Phe Asn Ala Gln Asn Asn
 165 170 175
 Gly Ser Asn Phe Gln Leu Glu Glu Ile Ser Arg Ala Gln Leu Val Pro
 180 185 190
 Leu Pro Pro Ser Thr Tyr Val Glu Phe Thr Val Ser Gly Thr Asp Cys
 195 200 205
 Val Ala Lys Glu Ala Thr Glu Ala Ala Lys Cys Asn Leu Leu Ala Glu
 210 215 220
 Lys Gln Tyr Gly Phe Cys Lys Ala Thr Leu Ser Glu Lys Leu Gly Gly
 225 230 235 240
 Ala Glu Val Ala Val Thr Cys Thr Val Phe Gln Thr Gln Pro Val Thr
 245 250 255
 Ser Gln Pro Gln Pro Glu Gly Ala Asn Glu Ala Val Pro Thr Pro Val
 260 265 270
 Val Asp Pro Asp Ala Pro Pro Ser Pro Pro Leu Gly Ala Pro Gly Leu
 275 280 285
 Pro Pro Ala Gly Ser Pro Pro Asp Ser His Val Leu Leu Ala Ala Pro
 290 295 300
 Pro Gly His Gln Leu His Arg Ala His Tyr Asp Leu Arg His Thr Phe
 305 310 315 320
 Met Gly Val Val Ser Leu Gly Ser Pro Ser Gly Glu Val Ser His Pro
 325 330 335
 Arg Lys Thr Arg Thr Val Val Gln Pro Ser Val Gly Ala Ala Ala Gly
 340 345 350
 Pro Val Val Pro Pro Cys Pro Gly Arg Ile Arg His Phe Lys Val
 355 360 365

<210> 58
 <211> 317
 <212> PRT
 <213> Rattus rattus

<400> 58
 Met Trp Leu Tyr Leu Leu Ala Leu Val Gly Leu Trp Asn Leu Leu Arg
 1 5 10 15
 Leu Phe Arg Glu Arg Lys Val Val Ser His Leu Gln Asp Lys Tyr Val
 20 25 30
 Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln
 35 40 45
 Leu Asp Arg Arg Gly Met Arg Val Leu Ala Ala Cys Leu Thr Glu Lys
 50 55 60
 Gly Ala Glu Gln Leu Arg Ser Lys Thr Ser Asp Arg Leu Glu Thr Val
 65 70 75 80
 Ile Leu Asp Val Thr Lys Thr Glu Ser Ile Val Ala Ala Thr Gln Trp
 85 90 95
 Val Lys Glu Arg Val Gly Asn Arg Gly Leu Trp Gly Leu Val Asn Asn
 100 105 110
 Ala Gly Ile Ser Val Pro Val Gly Pro Asn Glu Trp Met Arg Lys Lys
 115 120 125
 Asp Phe Ala Ser Val Leu Asp Val Asn Leu Leu Gly Val Ile Glu Val
 130 135 140
 Thr Leu Asn Met Leu Pro Leu Val Arg Lys Ala Arg Gly Arg Val Val
 145 150 155 160
 Asn Ile Ala Ser Thr Met Gly Arg Met Ser Leu Val Gly Gly Gly Tyr
 165 170 175
 Cys Ile Ser Lys Tyr Gly Val Glu Ala Phe Ser Asp Ser Leu Arg Arg
 180 185 190
 Glu Leu Thr Tyr Phe Gly Val Lys Val Ala Ile Ile Glu Pro Gly Gly

	195		200		205
Phe	Lys Thr Asn Val Thr Asn Met Glu Arg Leu Ser Asp Asn Leu Lys				
	210		215		220
Lys	Leu Trp Asp Gln Thr Thr Glu Glu Val Lys Glu Ile Tyr Gly Glu				
	225		230		235
Lys	Phe Gln Asp Ser Tyr Met Lys Ala Met Glu Ser Leu Val Asn Thr				
		245		250	255
Cys	Ser Gly Asp Leu Ser Leu Val Thr Asp Cys Met Glu His Ala Leu				
		260		265	270
Thr	Ser Cys His Pro Arg Thr Arg Tyr Ser Pro Gly Trp Asp Ala Lys				
		275		280	285
Phe	Phe Tyr Leu Pro Met Ser Tyr Leu Pro Thr Phe Leu Ser Asp Ala				
	290		295		300
Val	Ile His Trp Gly Ser Val Lys Pro Ala Arg Ala Leu				
	305		310		315

<210> 59
 <211> 356
 <212> PRT
 <213> Homo Sapiens

<400> 59

Met	Ser	Asp	Ser	Lys	Glu	Pro	Arg	Leu	Gln	Gln	Leu	Gly	Leu	Leu	Glu
1				5					10					15	
Glu	Glu	Gln	Leu	Arg	Gly	Leu	Gly	Phe	Arg	Gln	Thr	Arg	Gly	Tyr	Lys
			20					25					30		
Ser	Leu	Ala	Gly	Cys	Leu	Gly	His	Gly	Pro	Leu	Val	Leu	Gln	Leu	Leu
		35					40					45			
Ser	Phe	Thr	Leu	Leu	Ala	Gly	Leu	Leu	Val	Gln	Val	Ser	Lys	Val	Pro
	50					55					60				
Ser	Ser	Ile	Ser	Gln	Glu	Gln	Ser	Arg	Gln	Asp	Ala	Ile	Tyr	Gln	Asn
	65				70				75						80
Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Ser	Glu	Lys	Ser	Lys
			85					90					95		
Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly
		100					105					110			
Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr
		115				120					125				
Arg	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Leu	Gln
	130					135					140				
Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Trp	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu
	145				150				155						160
Pro	Glu	Lys	Ser	Lys	Met	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Arg	Leu
			165					170					175		
Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Gln	Gln	Glu	Ile
		180						185				190			
Tyr	Gln	Glu	Leu	Thr	Arg	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Pro	Glu
	195					200					205				
Lys	Ser	Lys	Gln	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Arg	Leu	Lys	Ala
	210					215					220				
Ala	Val	Gly	Glu	Leu	Pro	Glu	Lys	Ser	Lys	Gln	Glu	Ile	Tyr	Gln	
	225				230					235				240	
Glu	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Glu	Arg	Leu	Cys	His	Pro	Cys
			245					250					255		
Pro	Trp	Glu	Trp	Thr	Phe	Phe	Gln	Gly	Asn	Cys	Tyr	Phe	Met	Ser	Asn
		260						265					270		
Ser	Gln	Arg	Asn	Trp	His	Asp	Ser	Ile	Thr	Ala	Cys	Lys	Glu	Val	Gly
		275				280					285				
Ala	Gln	Leu	Val	Val	Ile	Lys	Ser	Ala	Glu	Glu	Gln	Asn	Phe	Leu	Gln
	290					295					300				

Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp
 305 310 315 320
 Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu
 325 330 335
 Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly
 340 345 350
 Glu Glu Asp Cys
 355

<210> 60
 <211> 23
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(23)
 <223> Xaa = Any Amino Acid

<400> 60
 Ile Tyr Gln Xaa Leu Thr Xaa Leu Lys Ala Ala Val Gly Glu Leu Xaa
 1 5 10 15
 Xaa Xaa Ser Lys Xaa Gln Xaa
 20

<210> 61
 <211> 202
 <212> PRT
 <213> Homo sapiens

<400> 61
 Met Cys Tyr Gly Lys Cys Ala Arg Cys Ile Gly His Ser Leu Val Gly
 1 5 10 15
 Leu Ala Leu Leu Cys Ile Ala Ala Asn Ile Leu Leu Tyr Phe Pro Asn
 20 25 30
 Gly Glu Thr Lys Tyr Ala Ser Glu Asn His Leu Ser Arg Phe Val Trp
 35 40 45
 Phe Phe Ser Gly Ile Val Gly Gly Gly Leu Leu Met Leu Leu Pro Ala
 50 55 60
 Phe Val Phe Ile Gly Leu Glu Gln Asp Asp Cys Cys Gly Cys Cys Gly
 65 70 75 80
 His Glu Asn Cys Gly Lys Arg Cys Ala Met Leu Ser Ser Val Leu Ala
 85 90 95
 Ala Leu Ile Gly Ile Ala Gly Ser Gly Tyr Cys Val Ile Val Ala Ala
 100 105 110
 Leu Gly Leu Ala Glu Gly Pro Leu Cys Leu Asp Ser Leu Gly Gln Trp
 115 120 125
 Asn Tyr Thr Phe Ala Ser Thr Glu Gly Gln Tyr Leu Leu Asp Thr Ser
 130 135 140
 Thr Trp Ser Glu Cys Thr Glu Pro Lys His Ile Val Glu Trp Asn Val
 145 150 155 160
 Ser Leu Phe Ser Ile Leu Leu Ala Leu Gly Gly Ile Glu Phe Ile Leu
 165 170 175
 Cys Leu Ile Gln Val Ile Asn Gly Val Leu Gly Gly Ile Cys Gly Phe
 180 185 190
 Cys Cys Ser His Gln Gln Gln Tyr Asp Cys
 195 200

<210> 62
 <211> 221
 <212> PRT
 <213> Mus musculus

<400> 62
 Met Glu Ala Gly Gly Val Ala Asp Ser Phe Leu Ser Ser Ala Cys Val
 1 5 10 15
 Leu Phe Thr Leu Gly Met Phe Ser Thr Gly Leu Ser Asp Leu Arg His
 20 25 30
 Met Gln Arg Thr Arg Ser Val Asp Asn Ile Gln Phe Leu Pro Phe Leu
 35 40 45
 Thr Thr Asp Val Asn Asn Leu Ser Trp Leu Ser Tyr Gly Val Leu Lys
 50 55 60
 Gly Asp Gly Thr Leu Ile Ile Val Asn Ser Val Gly Ala Val Leu Gln
 65 70 75 80
 Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Ser Pro Gln Lys His Gly
 85 90 95
 Val Leu Leu Gln Thr Ala Thr Leu Leu Ala Val Leu Leu Leu Gly Tyr
 100 105 110
 Gly Tyr Phe Trp Leu Leu Val Pro Asp Leu Glu Ala Arg Leu Gln Gln
 115 120 125
 Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser Pro
 130 135 140
 Leu Ala Asp Leu Ala Lys Ile Val Gln Thr Lys Ser Thr Gln Arg Leu
 145 150 155 160
 Ser Phe Ser Leu Thr Ile Ala Thr Leu Phe Cys Ser Ala Ser Trp Ser
 165 170 175
 Ile Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Ala Val Pro Asn Leu
 180 185 190
 Pro Gly Ile Leu Thr Ser Leu Ile Arg Leu Gly Leu Phe Cys Lys Tyr
 195 200 205
 Pro Pro Glu Gln Asp Arg Lys Tyr Arg Leu Leu Gln Thr
 210 215 220

<210> 63
 <211> 245
 <212> PRT
 <213> Cephalobidae elegans

<400> 63
 Met Asp Leu Glu Asn Phe Leu Leu Gly Ile Pro Ile Val Thr Arg Tyr
 1 5 10 15
 Trp Phe Leu Ala Ser Thr Ile Ile Pro Leu Leu Gly Arg Phe Gly Phe
 20 25 30
 Ile Asn Val Gln Trp Met Phe Leu Gln Trp Asp Leu Val Val Asn Lys
 35 40 45
 Phe Gln Phe Trp Arg Pro Leu Thr Ala Leu Ile Tyr Tyr Pro Val Thr
 50 55 60
 Pro Gln Thr Gly Phe His Trp Leu Met Met Cys Tyr Phe Leu Tyr Asn
 65 70 75 80
 Tyr Ser Lys Ala Leu Glu Ser Glu Thr Tyr Arg Gly Arg Ser Ala Asp
 85 90 95
 Tyr Leu Phe Met Leu Ile Phe Asn Trp Phe Phe Cys Ser Gly Leu Cys
 100 105 110
 Met Ala Leu Asp Ile Tyr Phe Leu Leu Glu Pro Met Val Ile Ser Val
 115 120 125
 Leu Tyr Val Trp Cys Gln Val Asn Lys Asp Thr Ile Val Ser Phe Trp
 130 135 140
 Phe Gly Met Arg Phe Pro Ala Arg Tyr Leu Pro Trp Val Leu Trp Gly

145		150		155		160
Phe	Asn	Ala	Val	Leu	Arg	Gly
		165				170
Leu	Val	Gly	His	Ala	Tyr	Phe
		180				185
Tyr	Gly	Val	Asp	Leu	Ile	Ser
		195				200
Pro	Asp	Glu	Asp	Gly	Gly	Ile
		210				215
Ala	Arg	Gln	Gln	Pro	Arg	Gly
		225				230
Arg	Leu	Gly	Gly	Asn		
				245		

<210> 64
 <211> 241
 <212> PRT
 <213> Cephalobidae elegans

<400> 64	
Met	Arg
1	5
Gly	Phe
	20
Asp	Gly
	35
Gly	Lys
	50
Met	Arg
	65
Glu	Glu
	80
Asp	Glu
	95
Glu	Arg
	110
Glu	Arg
	125
Ile	Glu
	140
Leu	Ile
	155
Ile	Asp
	170
Asn	Arg
	185
Asp	Asp
	200
Val	Ala
	215
Ala	Glu
	230
Glu	

<210> 65
 <211> 239
 <212> PRT
 <213> Sus scrofa

<400> 65


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Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu
1      5      10      15
Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
20      25      30
Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
35      40      45
Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp Asp Met Ala Ala Glu
50      55      60
Asp Val Ala Ala Thr Gly Ala Asp Pro Ser Glu Leu Glu Gly Gly Gly
65      70      75      80
Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu Leu Leu Leu Gly
85      90      95
Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly Asp Gln Pro Ala
100     105     110
Ala Ser Asp Ser Asp Asp Asp Glu Pro Pro Pro Leu Pro Arg Leu Lys
115     120     125
Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg Phe Asp Gly Val Gln
130     135     140
Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys Val Phe Asp Val Thr
145     150     155     160
Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro Tyr Gly Val Phe Ala
165     170     175
Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Glu
180     185     190
Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp Leu Thr Pro Ala Gln
195     200     205
Gln Glu Thr Leu Asn Asp Trp Asp Ser Gln Phe Thr Phe Lys Tyr His
210     215     220
His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu Pro Thr Val Tyr
225     230     235

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<210> 66
 <211> 499
 <212> PRT
 <213> Macaca fascicularis

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<400> 66
Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu Val
1      5      10      15
Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala Gly Ile
20      25      30
Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile
35      40      45
Val Asn Ser Gly Ser Leu His Glu Phe Met Asp Leu Ile Pro Asp Leu
50      55      60
Ala Val Glu Thr Trp Leu Leu Leu Ala Val Thr Leu Val Leu Leu Tyr
65      70      75      80
Leu Tyr Gly Thr His Ser His Gly Leu Phe Lys Lys Leu Gly Ile Pro
85      90      95
Gly Pro Thr Pro Leu Pro Leu Leu Gly Asn Ile Leu Ser Tyr Arg Lys
100     105     110
Gly Phe Trp Thr Asp Met Glu Cys Tyr Lys Lys Tyr Gly Lys Val Trp
115     120     125
Gly Phe Tyr Asp Gly Arg Gln Pro Val Leu Ala Ile Thr Asp Pro Asn
130     135     140
Met Ile Lys Thr Val Leu Val Lys Glu Cys Tyr Ser Val Phe Thr Asn
145     150     155     160
Arg Arg Pro Phe Gly Pro Val Gly Phe Met Lys Asn Ala Ile Ser Ile
165     170     175
Ala Glu Asp Glu Glu Trp Lys Arg Ile Arg Ser Leu Leu Ser Pro Thr

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<210> 67
<211> 457
<212> PRT
<213> Saccharomyces cerevisiae
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<400> 67															
Met	Gly	Arg	Trp	Ala	Leu	Asp	Val	Ala	Phe	Leu	Trp	Lys	Ala	Val	Leu
1				5					10					15	
Thr	Leu	Gly	Leu	Val	Leu	Leu	Tyr	Tyr	Cys	Phe	Ser	Ile	Gly	Ile	Thr
			20					25					30		
Phe	Tyr	Asn	Lys	Trp	Leu	Thr	Lys	Ser	Phe	His	Phe	Pro	Leu	Phe	Met
		35					40					45			
Thr	Met	Leu	His	Leu	Ala	Met	Asn	Arg	Thr	Val	Phe	Leu	Ala	Phe	Val
	50					55					60				
Phe	Gly	Trp	Tyr	Phe	Cys	Ser	Ile	Ala	Leu	Ser	Ile	Tyr	Asn	Arg	Trp
65					70					75				80	
Met	Phe	Asp	Pro	Lys	Asp	Gly	Leu	Gly	Ile	Gly	Tyr	Pro	Val	Leu	Val
				85					90					95	

Thr	Thr	Phe	His	Gln	Ala	Thr	Leu	Trp	Leu	Leu	Ser	Gly	Ile	Tyr	Ile		
			100					105					110				
Lys	Leu	Arg	His	Lys	Pro	Val	Lys	Asn	Val	Leu	Arg	Lys	Asn	Asn	Gly		
		115					120					125					
Phe	Asn	Trp	Ser	Phe	Phe	Leu	Lys	Phe	Leu	Leu	Pro	Thr	Ala	Val	Ala		
	130					135					140						
Ser	Ala	Gly	Asp	Ile	Gly	Leu	Ser	Asn	Val	Ser	Phe	Gln	Tyr	Val	Pro		
145					150					155					160		
Leu	Thr	Ile	Tyr	Thr	Ile	Ile	Lys	Ser	Ser	Ser	Ile	Ala	Phe	Val	Leu		
				165					170						175		
Leu	Phe	Gly	Cys	Ile	Phe	Lys	Leu	Glu	Lys	Phe	His	Trp	Lys	Leu	Ala		
			180					185							190		
Leu	Ser	Val	Ile	Ile	Met	Phe	Val	Gly	Val	Ala	Leu	Met	Val	Phe	Lys		
		195					200					205					
Pro	Ser	Asp	Ser	Thr	Ser	Thr	Lys	Asn	Asp	Gln	Ala	Leu	Val	Ile	Phe		
	210					215						220					
Gly	Ser	Phe	Leu	Val	Leu	Ala	Ser	Ser	Cys	Leu	Ser	Gly	Leu	Arg	Trp		
225					230					235					240		
Val	Tyr	Thr	Gln	Leu	Met	Leu	Arg	Asn	Asn	Pro	Ile	Gln	Thr	Asn	Thr		
			245						250						255		
Ala	Ala	Ala	Val	Glu	Glu	Ser	Asp	Gly	Ala	Leu	Phe	Thr	Glu	Asn	Glu		
			260					265							270		
Asp	Asn	Val	Asp	Asn	Glu	Pro	Val	Val	Asn	Leu	Ala	Asn	Asn	Lys	Met		
		275					280					285					
Leu	Glu	Asn	Phe	Gly	Glu	Ser	Lys	Pro	His	Pro	Ile	His	Thr	Ile	His		
	290					295					300						
Gln	Leu	Ala	Pro	Ile	Met	Gly	Ile	Thr	Leu	Leu	Leu	Thr	Ser	Leu	Leu		
305					310					315					320		
Val	Glu	Lys	Pro	Phe	Pro	Gly	Ile	Phe	Ser	Ser	Ser	Ile	Phe	Arg	Leu		
			325						330					335			
Asp	Thr	Ser	Asn	Gly	Gly	Val	Gly	Thr	Glu	Thr	Thr	Val	Leu	Ser	Ile		
			340					345					350				
Val	Arg	Gly	Ile	Val	Leu	Leu	Ile	Leu	Pro	Gly	Phe	Ala	Val	Phe	Leu		
		355					360					365					
Leu	Thr	Ile	Cys	Glu	Phe	Ser	Ile	Leu	Glu	Gln	Thr	Pro	Val	Leu	Thr		
	370					375					380						
Val	Ser	Ile	Val	Gly	Ile	Val	Lys	Glu	Leu	Leu	Thr	Val	Ile	Phe	Gly		
385					390					395					400		
Ile	Ile	Ile	Leu	Ser	Glu	Arg	Leu	Ser	Gly	Phe	Tyr	Asn	Trp	Leu	Gly		
			405						410					415			
Met	Leu	Ile	Ile	Met	Ala	Asp	Val	Cys	Tyr	Tyr	Asn	Tyr	Phe	Arg	Tyr		
			420					425					430				
Lys	Gln	Asp	Leu	Leu	Gln	Lys	Tyr	His	Ser	Val	Ser	Thr	Gln	Asp	Asn		
		435				440						445					
Arg	Asn	Glu	Leu	Lys	Gly	Phe	Gln	Asp									
	450					455											